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6, Appli
13, Appli
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1011.008 Million cell updates/sec
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Sequence 24, Appl
Sequence 11050, A
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Sequence 320, 1
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                                                                                                                                                  July 26, 2005, 15:58:52 ; Search time 30.7159 Seconds
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1 MKRERGALSRASRALRLAPF.....TAGVHIIREQDEAGPVEISA
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-906-125A-320
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US-09-905-381A-320
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US-09-905-381A-320
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Maximum Match 100%
Listing first 45 summaries
                                                                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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28 188.5 8.9 1091 3 US-08-986-485-5 Sequence 5, Appli 3 US-08-51.200-2 Sequence 2, Appli 3 187 8.8 340 4 US-09-651.200-2 Sequence 2, Appli 3 187 8.8 365 2 US-08-978-424-3 Sequence 3, Appli 3 187 8.8 365 3 US-09-288-383B-2 Sequence 2, Appli 3 187 8.8 365 4 US-09-249-016-6064 Sequence 2, Appli 3 187 8.8 270 4 US-09-551.200-4 Sequence 2, Appli 3 186.5 8.8 270 4 US-09-551.200-4 Sequence 24, Appli 3 186.5 8.8 270 4 US-09-551.200-4 Sequence 24, Appli 3 186.5 8.8 270 4 US-09-551.200-6 Sequence 26, Appli 3 186.5 8.8 270 4 US-09-551.200-6 Sequence 26, Appli 3 186.5 8.8 273 4 US-09-551.200-6 Sequence 26, Appli 4 1 180.5 8.5 365 4 US-09-651.200-6 Sequence 26, Appli 4 1 180.5 8.5 365 4 US-09-651.200-6 Sequence 24, Appli 4 1 180.5 8.5 365 4 US-09-611.748-24 Sequence 24, Appli 4 1 180.5 8.2 316 4 US-09-611.24 Sequence 24, Appli 4 173 8.2 316 4 US-09-611.24 Sequence 24, Appli 4 173 8.2 299 3 US-09-188-930-331 Sequence 331, Appli Appli 4 173 8.2 299 3 US-09-188-930-331
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ALIGNMENTS

Sequence 310, Application US/09907794A

Sequence 310, Application US/09907794A

APPLICANT: Genencech, Inc.

APPLICANT: Genencech, Inc.

APPLICANT: Berrara, Mary Entral, Avi

APPLICANT: Berrara, Mapoleone

APPLICANT: Generech, Inc.

APPLICANT: Gerein, Dan I.

APPLICANT: Gedwali, Paul J.

APPLICANT: Gedwali, Tox J.

APPLICANT: Gedwali, Tox J.

APPLICANT: Ban, James P.

APPLICANT: Milliams, P. Mickey

APPLICANT: Wood, Williams, P. Wickey

APPLICANT: Wood, Williams, P. Wickey

APPLICANT: WOOD WILLIAM, Berrara APPLICANTION NUMBER: 18/09/907,794A

CURRENT FILING DATE: 1999-07-28

FRIOR FELING DATE: 1999-07-28

FRIOR FILING DATE: 1999-07-28

FRIOR FILING DATE: 1999-09-11

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US-09-902-775A-320
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-07
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Patent No. 6664376
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hangpeter
Gerriteen, Mary E.
Goddard, A.
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Paoni, Nicholas F.
Roy, Margaret Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-907-794A-320
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPRENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
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PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 320
                                                                                                                                                                                                                                        PRIOR PELING TATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PLING DATE: 1999-07-07
PRIOR APLICATION NUMBER: US 60/145,698
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-07-28
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
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R FILING DATE: 1999-09-15

R FILING DATE: 1999-10-15

R RELING DATE: 1999-10-05

R PELING DATE: 1999-11-29

R PELING DATE: 1999-11-29

R PELING DATE: 1999-11-29

R PELING DATE: 1999-11-29

R PELING DATE: 1999-11-30
                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/US00/04414
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Best Local Similarity 31.7%
Matches 72; Conservative
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, ORGANISM: Homo Sapien
US-09-905-125A-320
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APPLICANT: Wood, William, I.
IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/902,775A

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR PILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR PILING DATE: 1999-07-08

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR APPLICATION NUMBER: PCT/US99/21990

PRIOR APPLICATION NUMBER: PCT/US99/21990

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-10-65

PRIOR PILING DATE: 1999-10-65
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PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-09-08
PRIOR PAPLICATION NUMBER: PCT/US99/20594
PRIOR PELING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-13
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PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-03
PRIOR PELING DATE: 1999-12-06
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PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
Sequence 320, Application US/09902775A
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
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Filvaroff, Ellen
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Paoni, Nicholas F.
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Gao, Wei-Qiang
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Eaton, Dan L.
                                                                                                             APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
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NUMBER OF SEQ ID NOS: 423
SEQ ID NO 320
LENGTH: 450
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ORGANISM: Homo Sapien
US-09-902-775A-320
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74 -DKPVTVVQSIGTEVIGTLRPDYRDRIRLF-ENGSLLLSDLQLADEGTYEVEISIT-DDT 130
                                                                                                                                                                                                                                                                                                                  131 FTGEKTINLTVDVPISRPQVLV-ASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLN 189
                                                                                                                                                                                                                      TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-11 2046-11 2046-11 2046-11 2000-09-18 PRIOR PELICATION NUMBER: US/09/906,700 CURRENT FILING DATE: 2000-09-18 PRIOR PELICATION NUMBER: PCT/US00/04414 PRIOR PILING DATE: 2000-02-22 PRIOR PELICATION NUMBER: US 60/143,048 PRIOR FILING DATE: 1999-07-07
                                                                                                                             17 LAPFVYLLLIOTDPLEGVNITSPVRLIHGTVGKSALLSVOYS--STSSDRPVVKWOLKR-
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  Length 450;
  13.3%; Score 282; DB 4; Length 45
31.7%; Pred. No. 1.2e-14;
ive 43; Mismatches 102; Indels
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PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR PILING DATE: 1999-09-13
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APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
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PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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Hillan, Kenneth,
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Mather, Jennie P.
Query Match
Best Local Similarity 31.7*
Matches 72; Conservative
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Botstein, David
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Gao, Wei-Qiang
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62 HTMPKYLLGSVNKSVVPDL--EYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGT 119
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                                                                                           TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same File Reference: GNE.1618P2C12
CURRENT APPLICATION NUMBER: US/09/903, 603A
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: PCT/US00/04414
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PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-07
PRIOR PLING DATE: 2000-01-05
NUMBER: PCT/US00/00219
PRIOR PELING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-0-07
PRIOR PELING DATE: 1999-07-07
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
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FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
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US-09-904-920A-320
; Sequence 320, Application US/09904920A
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Best Local Similarity 31.7%;
Matches 72; Conservative
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US-09-903-603A-320
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PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR PLILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-11-30
PRIOR PLILING DATE: 1999-11-30
PRIOR PRILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PLILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
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PRIOR PLILING DATE: 1999-12-06
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PRIOR PLILING DATE: 1999-12-06
PRIOR PLILING DATE: 1999-12-07
PRIOR PLILING DATE: 1999-12-20
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Patent No. 6767995
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Grimaldi, Christopher J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hangpeter
Gerritsen, Mary E.
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Hillan, Kenneth, J.
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Ither, Jennie P.
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Botstein, David
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Eaton, Dan L.
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US-09-906-700-320
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Best Local Similarity
Matches 72; Conserva
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US-09-903-603A-320
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Sequence 320, Application US/09909064
Patent No. 6818449
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Grimaldi, Christopher J.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerritsen, Mary E
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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PPLICANT: Wood, William, I.
(TLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
(TLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TILLE OF INVENTION:

TILLE FUER PRERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/904,920A

CURRENT FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-08

PRIOR PILING DATE: 1999-07-28

PRIOR PILING DATE: 1999-07-38

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-13

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-09-15

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-03

PRIOR PILING DAT
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Grimaldi, Christopher J.
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Hillan, Kenneth, J
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Pilvaroff, Ellen
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                                                 Dan L.
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; ORGANISM: Homo Sapien
US-09-904-920A-320
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                                                 Eaton,
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62 HTMPKYLLGSVNKSVVPDL--EYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGT 119
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                                                                                                                                                                                                                                                                        74 -DKPVTVVQSIGTEVIGTLRPDYRDRIRLF-ENGSLLLSDLQLADEGTYEVEISIT-DDT
                                                                                                                                    17 LAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYS--STSSDRPVVKWQLKR-
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                                                                       Gaps
Query Match 13.3%; Score 282; DB 4; Length 450; Best Local Similarity 31.7%; Pred. No. 1.2e-14; Matches 72; Conservative 43; Mismatches 102; Indels 10;
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CURRENT APPLICATION NUMBER: US/09/909,064
CURRENT FILING DATE: 2001-07-18
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PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
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PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR PLING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
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APPLICATION NUMBER: PCT/US99/21090
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APPLICATION NUMBER: PCT/US99/20944
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APPLICATION NUMBER: PCT/US99/23089
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PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 320
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Patent No. 6818746
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hangpeter
Gerritsen, Mary E.
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Stewart, Timothy A.
Tumas, Daniel
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Paoni, Nicholas F.
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Mather, Jennie P.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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US-09-909-064-320
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APPLICANT: WOOD, WILLIAM, 1.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPRENCE: 1046-14

CURRENT APPLICATION NUMBER: US/09/905,381A

CURRENT FILING DATE: 2001-07-13

PRIOR FILING DATE: 2000-02-22

PRIOR PLING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-06

PRIOR PLING DATE: 1999-07-26

PRIOR PLING DATE: 1999-07-26

PRIOR PLING DATE: 1999-07-28

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-09-15

PRIOR PLING DATE: 1999-09-15

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PRIOR PLING DATE: 1999-09-15
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PRIOR FILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR FILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1099-12-20
PRIOR PILING DATE: 1099-12-20
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 320
LENGTH: 450
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DR APPLICATION NUMBER: PCT/US99/23089

R FILING DATE: 1999-10-05

DR APPLICATION NUMBER: PCT/US99/28214

DR FILING DATE: 1999-11-29

DR APPLICATION NUMBER: PCT/US99/28313

DR FILING DATE: 1999-11-30

R FILING DATE: 1999-11-30

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US-09-906-618-320
Sequence 320, Application US/09906618
Partent No. 6828146
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CORGANISM: Homo Sapien
US-09-905-381A-320
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PPLICANT: Wood, William, I.
HTLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FITLE OF INVENTION: Acids Encoding the Same
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PRIOR PELICATION NUMBER: DCT/USO0/04414
PRIOR PELICATION NUMBER: DCT/USO0/04414
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR PELICATION NUMBER: US 60/146,222
PRIOR PELICATION NUMBER: US 60/146,222
PRIOR PELICATION NUMBER: US 60/146,222
PRIOR PELICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
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PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-0
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CURRENT FILING DATE: 2001-07-16
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Grimaldi, Christopher
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
Fong, Sherman
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Hillan, Kenneth, J.
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Gerritsen, Mary E
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Paoni, Nicholas F.
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Mather, Jennie P
                                     Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                                                                                                   Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                      Goddard, A.
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; ORGANISM: Homo Sapien
US-09-906-618-320
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                                                                                                                                                                                                                                                                                              131 FTGEKTINLTVDVPISRPQVLV-ASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLN 189
                                                                                                                                                                                                                                                                                                                          Sequence 5729, Application US/09513999C
; Sequence 5729, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Mine Edwards, J.B.
; APPLICANT: Duclert, J.Y.
; APPLICANT: Glordano, J.Y.
; TILE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; PILE REFERENCE: 59,US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 1090-02-26
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SEQ ID NO 5729
; LENGTH: 58
                                                                                                                                                                                  74 -DKPVTVVQSIGTEVIGTLRPDYRDRIRLF-ENGSLLLSDLQLADEGTYEVEISIT-DDT 130
                                                                                                               3 LKVPTTFLSPATGACSGLKVTVPSHTVHGVRGQALYLPVHYGFHTPASDIQII-WLFERP 61
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                                                                             17 LAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYS--STSSDRPVVKWQLKR-
                           10; Gaps
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Presenting Cell Driven Skin Conditions Using
Inhibitors of the CD2/LFA-3 Interaction
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                                                                                                                                                                                                                                                                                                                                                                                                     190 DSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVY 236
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                         Indels
; Pred. No. 1.2e-14; 43; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Wallner, Barbara P.
APPLICANT: Cooper, Kevin D.
TITLE OF INVENTION: Method of Pro-
TITLE OF INVENTION: Presenting C.
TITLE OF INVENTION: Inhibitors on NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 6, Application US/08466465; Patent No. 6162432
Best Local Similarity 31.7%
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Marches 58, Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-513-999C-5729
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Query Match

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Best Local Similarity
Matches 85; Conserva
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US-09-397-243D-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 VTVVQSIGTEVIGTLRPD-----YRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTF 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wallner, Barbara P.
Cooper, Kevin D.
TITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen
Presenting Cell Driven Skin Conditions Using
Inhibitors of the CD2/LFA-3 Interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 LAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKP
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SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08755
FILING DATE: 06-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/862,022
FILING DATE: 12-APR.1992
PRIOR APPLICATION NUMBER: US 07/770,969
FILING DATE: 07-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wyers, Louis (PLM)
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 36,965
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION FOR SEQ ID NO:
ERGOTEM TO THE TELECOMMUNICATION OF TELECOMMUNICATION OF
                                                                  APPLICATION NUMBER: US/08/466,465 FILING DATE:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 22.3%
Best Local Similarity 22.3%
Conservative
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251 FLLVTLVTVCACWKPSKRKQKKLEKQNSLEYMDQNDDRLKPEADTLPRSGEQERKNPMAL 310
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                                                                                                                                                                                                                                                                             Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US92/08755
FILING DATE: 06-OCT-1992
APPLICATION NUMBER: US 07/862,022
FILING DATE: 12-APR-1992
APPLICATION NUMBER: US 07/770,969
FILING DATE: 07-OCT-1991
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Myers, Louis (PLM)
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BGP-111CP
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/730,465 FILING DATE: 05-Dec-2000 PRIOR APPLICATION DATA:
                                                                                                                                    ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 351 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                STATE: Massachusetts
COUNTRY: USA
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US-08-986-485-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.5%; Score 202; DB 4; Length 31.
22.7%; Pred. No. 2.2e-08;
ive 66; Mismatches 148; Indels
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APPLICANT: WU, SHUJIAN
APPLICANT: WWW. SHUJIAN
APPLICANT: TRUNEH, ALEMSEGED
TITLE OF INVENTION: A HUMAN LIG-1 HOMOLOG (HLIG-1)
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAINER & PRESTIA
STREET: P.O. BOX 980
                                                                                           APPLICANT: Cornecki, Elizabeth
APPLICANT: Schocka, Malgorzata B.
TITLE OF INVENTION: Human Platelet F11 Receptor
FILE REPERENCE: 011.0021
CURRENT APPLICATION NUMBER: US/09/397,243D
RIOR APPLICATION NUMBER: 05/09.16
PRIOR APPLICATION NUMBER: 60/100,638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OMERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
OFFICE FASTES FOR MINDOWS VERSION 2.0
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APPLICATION NUMBER: US/08/986,485
FILING DATE: 08-DEC-1997
Sequence 13, Application US/09397243D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-08-986-485-2
; Sequence 2, Application US/08986485
; Patent No. 6046030
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ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 22.73
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-09-397-243D-13
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COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 AFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENP 222
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Patent No. 6210921

GENERAL INFORMATION:
APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
TITLE OF INVENTION: CAR, A No. 6210921el Coxsackievirus and Adenovirus
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 ENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLELSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
9.4%; Score 199.5; DB 3;
Best Local Similarity 21.3%; Pred. No. 2.1e-07;
Matches 84; Conservative 58; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 -----YPRSPARSPATGRIHSSPPRAPSSP 385
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                                60/059,448
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,44,
FILING DATE: 22-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFRENCE/DOCKET NUMBER: GH-7
TELECOMMUNICATION:
TELEPHONE: 610-407-0700
                                                                                                                                                                                                            TELEFAX: 610-40.
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
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ADDRESSEE: LAHIVE &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279 ------BDVPPPKSRTSTARSYIGSNHSSLGSMSSNM 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 9.3%; Score 197.5; DB 3; Length 365; Best Local Similarity 23.5%; Pred. No. 6.2e-08; Matches 91; Conservative 66; Mismatches 146; Indels 85; Gaps
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,383B
FILING DATE: 12-SEP-1997
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 60/026,100
FILING DATE: 13-SEP-1996
ATTORNEY AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REFERENCE/DOCKET NUMBER: DFN-020
TELEPHONE: (617)227-7400
TELEPHONE: (617)742-4214
INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acide
TYPE: amino acide
TOPOLOGY: linear
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Search completed: July 26, 2005, 16:15:52 Job time : 31.7159 secs Sequence

Sequence 6, Appli Sequence 320, App Sequence 320, App

Scoring table:

Searched:

Database

Perfect score:

Sequence:

OM protein

Run on:

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1 MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 2122; DB 16; Length 416; 100.0%; Pred. No. 3.3e-138; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Davids, Andrew Robert
APPLICANT: Bagan, Richard Joseph
APPLICANT: Pagan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Power, Christine
APPLICANT: Chvatchko, Yolande
APPLICANT: Chvatchko, Yolande
APPLICANT: Chvatchko, Yolande
APPLICANT: Chvatchko, Yolande
TILE OF INVENTION: Cytokine antagonist molecules
FILE REFERENCE: 674582-2001
CURRENT APPLICATION UNMBER: US/10/706,691
CURRENT APPLICATION NUMBER: PCT/GB03/01851
PRIOR APPLICATION NUMBER: CT/GB03/01851
PRIOR FILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 43
SOFTWARE: SeqWin99, version 1.02
SEQ ID NO 16
6 US-10-706-691-4

6 US-10-706-691-14

6 US-10-706-691-14

1 US-09-909-320-320

US-09-909-320-320

US-09-902-853-320

US-09-907-841-320

US-09-903-746-320

US-09-903-746-320

US-09-903-748-320

US-09-903-748-320

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Publication No. US20040204352A1
GENERAL INFORMATION:
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        TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Simil
Matches 416; C
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1519.387 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16, P
Sequence 41, P
Sequence 18, P
Sequence 26, P
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Sequence 20,
Sequence 43,
Sequence 836
Sequence 7,
Sequence 22,
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                                                                                                              July 26, 2005, 16:01:42 ; Search time 106.504 Seconds
                                                                                                                                                                                            2122
1 MKRERGALSRASRALRLAPF......TAGVHIIREQDEAGPVEISA
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-706-691-41
US-10-706-691-18
US-10-706-691-26
US-10-706-691-20
US-10-706-691-43
US-10-112-944-434
US-10-112-944-880
US-10-415-188-7
US-10-415-188-7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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241 LYIILSTGGIFLLVTLVTVCACWKPSKRKQKKLEKQNSLEYMDQNDDRLKPEADTLPRSG 300
241 LYIILSTGGIFLLVTLVTVCACWKPSKRKQKKLEKQNSLEYMDQNDDRLKPEADTLPRSG 300
                                                                                   301 EQERKNOPMALYILKDKDSPETEENPAPEPRSATEPGPPGYSVSPAVPGRSPGLPIRSARR 360
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                                                                  EQERKNPMALYILKDKDSPETEENPAPEPRSATEPGPPGYSVSPAVPGRSPGLPIRSARR
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                                                                                                                                   361 YPRSPARSPATGRTHSSPPRAPSSPGRSRSASRTLRTAGVHIIREQDEAGPVEISA 416
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Sequence 18, Application US/10706691

Sequence 18, Application US/10706691

GENERAL INFORMATION:
APPLICANT: Davids, Andrew Robert
APPLICANT: Pagan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Power, Christine
APPLICANT: Boschert, Ursula
TITLE OF INVENTION: Cytckine antagonist molecules
FILE REFERENCE: 67458-2001
CURRENT APPLICATION NUMBER: US/10/706,691
CURRENT APPLICATION NUMBER: 2003-11-12
PRIOR APPLICATION NUMBER: GB 0209884.6
PRIOR APPLICATION NUMBER: GB 0209884.6

PRIOR APPLICATION NUMBER: GB 0209884.6

PRIOR APPLICATION NUMBER: GB 0209884.6

SEQ ID NOS: 43

SOFTWARE: SeqWin99, version 1.02
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ORGANISM: Homo sapiens
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                                     LKDGKPLLNDSRMLLSPDOKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSS 240
                                                                                                                                                                                                                                      EQERKNPMALYILKDKDSPETEENPAPEPRSATEPGPPGYSVSPAVPGRSPGLPIRSARR 360
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100.0%; Pred. No. 3.3e-138;
tive 0; Mismatches 0;
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Publication No. US20040204352A1
GENERAL INFORMATION:
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US-10-706-691-41
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Best Local Simi
Matches 416;
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 LYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACWKPSKRKQKKL 273
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Sequence 26, Application US/10706691
Fublication No. US20040204352A1
GENERAL INFORMATION:
APPLICANT: Davids, Andrew Robert
APPLICANT: Pagan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Power. Christine
APPLICANT: Chvatchko, Yolande
APPLICANT: Chvatchko, Yolande
APPLICANT: Boschert, Ursula
TITLE OF INVENTION: Cytokine antagonist molecules
FILE REFERENCE: 674582-2001
CURRENT APPLICATION NUMBER: PCT/GB03/01851
PRIOR FILING DATE: 2003-11-12
PRIOR PLICATION NUMBER: PCT/GB03/01851
PRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 43
SOFTWARE: SeqWin99, version 1.02
SEQ ID NO 25
SEQ ID NO 25
LENGTH: 383
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; ORGANISM: Homo sapiens
US-10-706-691-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040043424A1 5831801CD1
US-10-432-103-4
                       APPLICANT: GANDHI, Ameena R.
APPLICANT: ARVIZU, Chandra
APPLICANT: ARVIZU, Chandra
APPLICANT: YAO, Monique G.
TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS
FILE REPERENCE: PF-0641 PCT.
CURRENT APPLICATION NUMBER: US/10/432,103
CURRENT FILING DATE: 2003-05-16
PRIOR FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PERL PROGRAM
SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y GENERAL INFORMATION:

APPLICANT: Fagan, Richard Joseph
APPLICANT: Fagan, Richard Joseph
APPLICANT: Pabelps, Christopher Benjamin
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Power, Christine
APPLICANT: Chvatchko, Yolande
APPLICANT: Boschert. Ursula
TITLE OF INVENTION: Cyclokine antagonist molecules
FILE REFERENCE: 674582-2001
CURRENT APPLICATION NUMBER: PCT/GB03/01851
FRIOR PELING DATE: 2003-11-12
PRIOR FILING DATE: 2003-04-30
FRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 43
SOFTWARE: SeqWin99, version 1.02
SEQ ID NO. SEQ ID NOS: 43
SEQ ID NO. SEQ ID NOS: 43
SEQ ID NO. SEQ ID NOS: 43
CRANISH: HOMO SADIENB
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; Sequence 20, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
GURURAJAN, Rajagopal
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Publication No. US20040048249A1
GENERAL INFORMATION:
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                                                                Gaps
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                  Length 240;
                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 43, Application US/10706691

Sequence 43, Application US/10706691

GENERAL INFORMATION:

APPLICANT: Fagan, Richard Joseph

APPLICANT: Phelps, Christopher Benjamin

APPLICANT: Phelps, Christopher Benjamin

APPLICANT: Phelps, Christopher Benjamin

APPLICANT: Christine

APPLICANT: Chartchko, Yolande

APPLICANT: Boschert, Ursula

TITLE OF INVENTION: Cytckine antagonist molecules

FILE REFERENCE: 674582-2001

CURRENT APPLICATION NUMBER: US/10/706,691

CURRENT FILING DATE: 2003-11-12

PRIOR APPLICATION NUMBER: GB 0209884.6

PRIOR FILING DATE: 2003-04-30

NUMBER OF SEQ ID NOS: 43

SEQ ID NO 43

LENTHR: 246

TUND: CHRISTOPH: 246

TUND: CHRISTOPH: 246
                  56.8%; Score 1205; DB 16;
100.0%; Pred. No. 3.4e-75;
iive 0; Mismatches 0;
                                                                Matches 240; Conservative
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Best Local Similarity 100.
Matches 240; Conservative
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ORGANISM: Homo sapiens
                  Query Match
Best Local Similarity
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US-10-706-691-43
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181 LKDGKPLLNDSRMLLSPDQKVLTITRVLMBDDDLYSCMVBNPISQGRSLPVKITVYRRSS 240
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", Sequence 880, Application US/10112944

; Publication No. US20040048249A1

; GENERAL INFORMATION:
APPLICANT: Tang, Y: Tom
APPLICANT: Yang, Yonghong
APPLICANT: Weng, Gezhi
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Ren, Feiyan
APPLICANT: Weng, Jian-Rui
APPLICANT: Wang, Junrui
APPLICANT: Zhao, Qing A.
APPLICANT: Kang, Zhiwei
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Best Local Similarity 96.79
Matches 236; Conservative
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ORGANISM: Homo sapiens
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RESULT 8 US-10-112-944-434 ; Sequence 434, Application US/10112944

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1, Narinder K.; ARVIZU, Chandra S.;
Y. Tom; LU, Dyung Aina M.;
I, Brendan M.; BAUGHN, Mariah R.;
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                                                                                                                                                          APPLICANT: Zhao, Qing A. APPLICANT: Wang, Zhiwei TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and TITLE OF INVENTION: Secreted Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
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Pred. No. 2.7e-73;
4; Mismatches 3;
                                                                                                                                                                                                                                            CURRENT FILING DATE: 2002-03-28

PRIOR APPLICATION NUMBER: US/10/112,944

PRIOR APPLICATION NUMBER: US 09/488,725

PRIOR FILING DATE: 2000-01-21

PRIOR FILING DATE: 2000-01-25

PRIOR FILING DATE: 2000-02-03

PRIOR PELICATION NUMBER: US 09/496,914

PRIOR PELICATION NUMBER: US 09/515,126

PRIOR PELING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: US 09/519,705

PRIOR PLILING DATE: 2000-03-07

PRIOR PLILING DATE: 2000-03-07

PRIOR APPLICATION NUMBER: US 09/540,217

PRIOR APPLICATION NUMBER: US 09/540,217

PRIOR APPLICATION NUMBER: US 09/552,929
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Publication No. US20040049010A1
GENERAL INFORMATION:
APPLICANT: WARREN, Bridget A.; XU, Yuming;
APPLICANT: YUE, Henry; BATRA, Sajeev;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 09/577,408
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 924
SOFTWARE: Dt_genes Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.5%;
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Best Local Similarity 97.1'
Matches 234; Conservative
                                                  Ren, Feiyan.
Xue, Aidong J.
Wang, Jian-Rui
Wehrman, Tom
                                                                                                                        Ghosh, Malabika
                                                                                                                                           Wang, Dunrui

// TYPE: PRT
// ORGANISM: Homo sapiens
US-10-112-944-880

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US-10-415-188-7
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                                                                                                                                                                                                                                                                              1 MLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFL
                                                                                                                                                                                                                                                                                                                                                                       253 LVTLVTVCACWKPSKRKQKKLEKQNSLEYMDQNDDRLKPEADTLPRSGEQERKNPMALYI
                                                                                                                                                                                                                                              193 MLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFL
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                                                                                                                            Length 224;
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; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040049010A1 382654CD1
US-10-415-188-7
                                                                                                                                                                                     Indels
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                                                                                                                        Query Match 54.5%; Score 1157; DB 15; Best Local Similarity 100.0%; Pred. No. 6.5e-72; Matches 224; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Davids, Andrew Robert
APPLICANT: Pagan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Phelps, Christine
APPLICANT: Chvatchko, Yolande
APPLICANT: Boschert, Ursula
APPLICANT: ATTLE OF INVENTION: Cytokine antagonist molecules
FILE REFERENCE: 674582-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/706,691 CURRENT FILING DATE: 2003-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22, Application US/10706691
Publication No. US20040204352A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 213
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                                                                                                                                                                                                                                                                                                                                                                  1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 PLEGVNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIG 89
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                                                                                                                                                                                                                                 Length 207;
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                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/10706691
; Sequence 4, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
    APPLICANT: Davids, Andrew Robert
; APPLICANT: Phelps, Christoher Benjamin
APPLICANT: Phelps, Christoher Benjamin
APPLICANT: Power, Christoher Benjamin
APPLICANT: Chartchko, Yolande
; APPLICANT: Chartchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10/706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SEQ ID NOS: 43
; SEQ ID NOS: 43
; SEQ ID NOS: 43
                                                                                                                                                                                                                               Score 1045; DB 16;
Pred. No. 3.2e-64;
                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 3.2.
Matches 207; Conservative 0; Mismatches
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PRIOR APPLICATION NUMBER: GB 0209884.6
PRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 43
SCFTWARE: SeqWin99, version 1.02
SEQ ID NO 22
LENGTH: 207
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ORGANISM: Homo sapiens
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US-10-706-691-22
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US-10-706-691-4
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RESULT 13 US-10-706-691-24

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 25.8%; Score 548; DB 16; Length 110; Best Local Similarity 100.0%; Pred. No. 2.9e-30; Matches 110; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/10706691

| Sequence 14, Application US/10706691
| Publication No. US20040204352A1
| GENERAL INFORMATION:
| APPLICANT: Davids, Andrew Robert
| APPLICANT: Pagen, Richard Joseph
| APPLICANT: Phelps, Christopher Benjamin
| APPLICANT: Power, Christopher Benjamin
| APPLICANT: Chvatchko, Yolande
| APPLICANT: Construction Construction Current Construction NUMBER: US/10/706,691
| CURRENT FILING DATE: 2003-11-12
| PRIOR FILING DATE: 2003-04-30
| SOFTWARE: SeqWin99, version 1.02
| JENGTHARE: SeqWin99, version 1.02
                   Sequence 24, Application US/10/00031

GENERAL INFORMATION: US/20040204552A1

GENERAL INFORMATION: US/20040204552A1

GENERAL INFORMATION: Andrew Robert

APPLICANT: Pagan, Richard Joseph

APPLICANT: Phalps, Christopher Benjamin

APPLICANT: Power, Christine

APPLICANT: Chvatchko, Yolande

APPLICANT: Chvatchko, Yolande

APPLICANT: Chvatchko, Yolande

APPLICANT: Gracher, Ursula

TITLE OF INVENTION: Cytokine antagonist molecules

FILE REFERENCE: 674562-2001

CURRENT APPLICATION NUMBER: US/10/706,691

CURRENT FILING DATE: 2003-11-12

PRIOR FILING DATE: 2003-04-30

PRIOR FILING DATE: 2002-04-30

PRIOR FILING DATE: 2002-04-30

NUMBER OF SEQ ID NOS: 43

SOFTWARE: SeqMin99, version 1.02

SEQ ID NO 24

LENGTH: 110
Application US/10706691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
US-10-706-691-24
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US-10-706-691-14
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Query Match 22.8%; Score 484; DB 16; Length 94; Best Local Similarity 100.0%; Pred. No. 6.3e-26; Matches 94; Conservative 0; Mismatches 0; Indels
                                 61 SPPRAPSSPGRSRSASRTLRTAGVHIIREQDEAGPVEISA 100
377 SPPRAPSSPGRSRSASRTLRTAGVHIIREQDEAGPVEISA 416
                                                                                                                                                              Sequence 6, Application US/10706691
; Sequence 6, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Power, Christine
; APPLICANT: Power, Christine
; APPLICANT: Power, Vichard Dapping Mapplicant
; APPLICANT: Power, Vichard
; APPLICANT: Chartche, Yolande
; APPLICANT: Chartche, Yolande
; APPLICANT: Chartche, Usula
; TITLE OF INVENTION: Cytokine antagonist molecules
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/GB03/01851
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR PILING DATE: 2002-04-30
; NUMBER: OF SEQ ID NOS: 43
; SCOTWARE: SeqWin99, version 1.02
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CRGANISM: Homo sapiens
US-10-706-691-6
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US-10-706-691-6
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Search completed: July 26, 2005, 16:21:17 Job time : 108.504 secs

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Maximum Match 100%
Listing first 45 summaries
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seq length: 2000000000
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1: /cgn2 6/ptodata/2/pubpaa/US07

1: /cgn2 6/ptodata/2/pubpaa/PCT N

2: /cgn2 6/ptodata/2/pubpaa/PCT N
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/ Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB_pep:*
/ Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB_pep:*
/ Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB_pep:*
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/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                 US-10-706-691-20

US-10-706-691-43

US-10-432-103-4

US-10-706-691-16

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US-10-112-944-434

US-10-112-944-880

US-10-706-691-18

US-10-706-691-26
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               Sequence 20, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 16, Appl
Sequence 11, Appl
Sequence 434, App
Sequence 880, App
Sequence 22, Appl
Sequence 26, Appl
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US-09-905-056-320	03-5	US-09-902-692-320	-09-907-925-32	-32	US-09-903-943-320	US-09-907-794-320	-09-902-736-	-09-904-956-3	US-09-904-119-320	-749A	-903-3	-78	9	46-	US-09-904-786-320	4-820-3	US-09-909-204-320	US-09-904-859-320	US-09-907-942-320	'n	US-09-906-838-320	6-742-	US-09-908-093-320	03-640-3	-904-011-3	907-84	-09-907-824-3	902-853-32	•	-088B-	09-909-320-3	-10-706-69	91-
	e 320,	320,	Φ	e 320,	e 320,	e 320,	e 320,	e 320,	Φ	e 320,	e 320,	e 320,	320,	320,	320,	æ	e 320,	e 320,	e 320,	e 320,	e 320,	e 320,	e 320,	e 320,	ce 320,	4.5	320,	320,	320,	320,	w		24,

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RESULT 1 US-10-706-691-20

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-20
                                                                                           Query Match
Best Local S
Matches 240
                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: GB 0209884.6
PRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 43
SOFTWARE: SegWin99, version 1.02
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Davids, Andrew Robert
APPLICANT: Fagan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Power, Christine
APPLICANT: Chvatchko, Yolande
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/10706691 Publication No. US20040204352A1
                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/706,691
CURRENT FILLING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/GB03/01851
PRIOR FILING DATE: 2003-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chvatchko, Yolande
APPLICANT: Boschert, Ursula
TITLE OF INVENTION: Cytokine antagonist molecules
FILE REFERENCE: 674582-2001
                                                                                        y Match 100.0%; Score 1205; DB 16; Local Similarity 100.0%; Pred. No. 5.5e-102; hes 240; Conservative 0; Mismatches 0;
                        MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST
MKRERGALSRASRALKLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST 60
                                                                                             Indels
                                                                                                                                       Length 240;
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                                                                                           Gaps
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APPLICANT: Pagan, Richard Joseph
APPLICANT: Pagan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Power, Christopher
APPLICANT: Chvatchko, Yolande
APPLICANT: Boschert, Ursula
TITLE OF INVENTION: Cytokine antagonist molecules
FILE REFERENCE: 674582-2001
CURRENT APPLICATION NUMBER: PCT/GB03/01851
PRIOR APPLICATION NUMBER: PCT/GB03/01851
PRIOR APPLICATION NUMBER: PCT/GB03/01851
PRIOR APPLICATION NUMBER: GD 0209884.6
PRIOR FILING DATE: 2003-04-30
PRIOR FILING DATE: 2002-04-30
ORUNBER OF SEQ ID NOS: 43
SOCTWARE: SeqWin99, version 1.02
SEQ ID NO 43
LENGTH: 246
TYPE: PRT
ORGANISM: Homo sapiens
US-10-706-691-43
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US-10-432-103-4
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                                                                                                                               Sequence 4, Application US/10432103 Publication No. US20040043424A1 GENERAL INFORMATION:
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Best Local Similarity
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                  APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: BAUGHN, MATIAR R.
APPLICANT: LU, Dyung Aina M.
APPLICANT: YUE, Henry
APPLICANT: ELLICTT, Vicki S.
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LU, Dyung Aina M.
YUE, Henry
ELLIOTT, Vicki S.
THANGAVELU, Kavitha
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APPLICANT: Davids, Andrew Robert
APPLICANT: Fagan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Phelps, Christopher
APPLICANT: Power, Christine
APPLICANT: Chratchko, Yolande
APPLICANT: Boschert, Ursula
TITLE OF INVENTION: Cytokine antagonist molecules
FILE REFERENCE: 674582-2001
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: US/10/706,691
CURRENT FILING DATE: 2003-04-30
PRIOR APPLICATION NUMBER: GD 2009884.6
PRIOR FILING DATE: 2002-04-30
PRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 43
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US-10-706-691-16
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CURRENT FILING DATE: 2003-05-16
PRIOR APPLICATION NUMBER: 60/249,645
PRIOR FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PERL Program
SEQ ID NO 4
                                                                               SOFTWARE: SeqWin99,
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/10706691
Publication No. US20040204352A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 240; Conserv
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Best Local :
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APPLICANT: ARVIZU, Chandra
APPLICANT: YAO, Monique G.
TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS
FILE REFERENCE: PF-0841 PCT
                 LENGTH: 416
TYPE: PRT
ORGANISM: Homo s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20040043424A1 5831801CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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GURURAJAN, Rajagopal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAMKUMAR,
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                                                                                                    version 1.02
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Pred. No. 7.4e-102;
; Mismatches 0;
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Query Match

100.0%;

Score 1205;

DB 16;

Length 416;

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RESULT 6
US-10-112-944-434
; Sequence 434, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
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US-10-706-691-41
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                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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PRIOR FILING DATE: 2003-04-30
PRIOR APPLICATION NUMBER: GB 0209884.6
PRIOR RILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 43
SOFTMARE: SegWin99, version 1.02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Chvatchk, Yolande
APPLICANT: Boschert, Ursula
TITLE OF INVENTION: Cytokine antagonist molecules
FILE REFERENCE: 674582-2001
CURRENT APPLICATION NUMBER: US/10/706,691
CURRENT FILING DATE: 2003-11-12
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APPLICANT: Fagan, Richard Joseph
APPLICANT: Phelps, Christopher Be
APPLICANT: Power, Christine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 416
                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 100.0%; Score 1205; DB 16;
Local Similarity 100.0%; Pred. No. 1.2e-101;
les 240; Conservative 0; Mismatches 0;
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US-10-112-944-880

Sequence 880, Application US/10112944 Publication No. US20040048249A1 GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom APPLICANT: Yang, Yonghong

Yang, ic., Weng, Gezhi

APPLICANT: APPLICANT: APPLICANT:

Zhang, Jie Ren, Feiyan Xue, Aidong

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CURRENT APPLICATION NUMBER: US/10/112,944

CURRENT FILING DATE: 2002-03-28

PRIOR APPLICATION NUMBER: US 09/488,725

PRIOR FILING DATE: 2000-01-21

PRIOR FILING DATE: 2000-01-21

PRIOR FILING DATE: 2000-01-25

PRIOR FILING DATE: 2000-02-03

PRIOR FILING DATE: 2000-02-03

PRIOR FILING DATE: 2000-02-03

PRIOR FILING DATE: 2000-02-03

PRIOR APPLICATION NUMBER: US 09/515,126

PRIOR APPLICATION NUMBER: US 09/519,705

PRIOR FILING DATE: 2000-03-07

PRIOR FILING DATE: 2000-03-07

PRIOR FILING DATE: 2000-03-07

PRIOR FILING DATE: 2000-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: pt_FL_genes Version 5.0
SEQ_ID_NO_434
                                                                                                                                                                                                                                                                                                                                    Matches 233;
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Best Local Similarity
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APPLICANT: Zhao, Oing A.
APPLICANT: Wang, Zhiwei
TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
TITLE OF INVENTION: Secreted Polypeptides
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PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 924
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PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 09/552,929
PRIOR FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 256
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                   EVEISITODTFTGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTW
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LKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLDSCVVENPINQGRTLPCKITVYKKSS
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Xue, Aidong J.
Wang, Jian-Rui
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Weng, Gezhi
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97.1%;
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Pred. No. 4.1e-99;
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APPLICANT: Davids, Andrew Robert
APPLICANT: Fagan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Power, Christine
APPLICANT: Chvatchko, Yolande
APPLICANT: Chvatchko, Yolande
APPLICANT: Boschert Ursula
ITITLE OF INVENTION: Cytokine antagonist molecules
FILE REFERENCE: 674592-2001
CURRENT APPLICATION NUMBER: US/10/706,691
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/GB03/01851
PRIOR APPLICATION NUMBER: PCT/GB03/01851
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                                                                                                                                                                                                                                                   Sequence 18, Application US/10706691 Publication No. US20040204352A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 924
SOFTWARE: Dt FL genes Version
SEQ ID NO 880
LENGTH: 256
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APPLICANT: Wang, Zhiwei
TITLE OF INVENTION: No. US20040048249Alel Nucleic
TITLE OF INVENTION: Secreted Polypeptides
FILE REFERENCE: 805A
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APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 09/552,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 09/577,408
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CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
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PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR FILING DATE: 2000-02-28
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Wehrman, Tom
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97.1%;
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Pred. No. 4.1e-99;
4; Mismatches 3;
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; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-18
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US-10-706-691-22
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SEQ ID NO 22
LENGTH: 207
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Publication No. US20040204352A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                             Query Match
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Best Local Similarity
Matches 234; Conserv
                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 674582-2001
CURRENT APPLICATION NUMBER: US/10/706,691
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/GB03/01851
PRIOR FILING DATE: 2003-04-30
PRIOR APPLICATION NUMBER: GB 0209884.6
PRIOR FILING DATE: 2002-04-30
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PRIOR FILING DATE: 2002-04-30
NUMBER OF SEO ID NOS: 43
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APPLICANT: Boschert, Ursula
TITLE OF INVENTION: Cytokine antagonist molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Davids, Andrew Robert
APPLICANT: Fagan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Power, Christine
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                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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nes 207; Conserv
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                                                                        61 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA
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                                                                                            | DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSS
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STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD
                     STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRWLLSPDQKVLTITRVLMEDDD 213
                                                                                                                                                 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 60
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                                                                                                                                                                                                                        86.7%; So llarity 100.0%; I Conservative 0;
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Pred. No. 1.5e-98;
                                                                                                                                                                                                                                                             DB 16;
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                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                             Length 207;
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240

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; Sequence 4, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
APPLICANT: Davids, Andrew Robert
APPLICANT: Fagan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Power, Christine
APPLICANT: Chvatchko, Yolande
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Davids, Andrew Robert
APPLICANT: Fagan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Phelps, Christopher
APPLICANT: Phelps, Christine
APPLICANT: Chratchko, Yolande
APPLICANT: Boschert, Ursula
TITLE OF INVENTION: Cytokine antagonist molecules
FILE REFERENCE: 674582-2001
CURRENT APPLICATION NUMBER: US/10/706,691
CURRENT APPLICATION NUMBER: PCT/GB03/01851
PRIOR APPLICATION NUMBER: PCT/GB03/01851
PRIOR APPLICATION NUMBER: GB 0209884.6
PRIOR APPLICATION NUMBER: GB 0209884.6
PRIOR APPLICATION NUMBER: GB 0209884.6
PRIOR TILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 43
SOFTWARE: SegWin99, version 1.02
APPLICANT: Power, Christine
APPLICANT: Chratchko, Yolande
APPLICANT: Chratchko, Yolande
APPLICANT: Beschert, Ursula
TITLE OF INVENTION: Cytokine antagonist molecules
FILE REFERENCE: 674582-2001
CURRENT APPLICATION NUMBER: US/10/706,691
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/GB03/01851
PRIOR FILING DATE: 2003-04-30
PRIOR FILING DATE: 2003-04-30
PRIOR FILING DATE: 2002-04-30
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; ORGANISM: Homo sapiens
US-10-706-691-26
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Best Local Similarity 100.0%; Pred. No. 4.0
Matches 207; Conservative 0; Mismatches
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LENGTH: 383
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; Pred. No. 4.6e-87;
0; Mismatches 0;
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APPLICANT: Davids, Andrew Robert
APPLICANT: Fagan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Power, Christopher
APPLICANT: Power, Christine
APPLICANT: Boschert, Ursula
TITLE OF INVENTION: Cytokine antagonist molecules
FILE REFERENCE: 674582-2001
CURRENT APPLICATION NUMBER: US/10/706,691
CURRENT FILING DATE: 2003-01-12
PRIOR APPLICATION NUMBER: PCT/GB03/01851
PRIOR APPLICATION NUMBER: GB 0209884.6
PRIOR PILING DATE: 2003-04-30
PRIOR PILING DATE: 2002-04-30
                                                                                                                                                                                                                                               RESULT 13
US-10-706-691-6
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-24
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US-10-706-691-24
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                                                                                                                                                                     Sequence 6, Application US/10706691
Publication No. US20040204352A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 45.5%; Score 548; DB 16; Best Local Similarity 100.0%; Pred. No. 2.8e-42; Matches 110; Conservative 0; Mismatches 0;
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SOFTWARE: SegWin99, vers
SEQ ID NO 4
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Publication No. US20040204352A1
                                                APPLICANT: Davids, Andrew Robert
APPLICANT: Fagan, Richard Joseph
APPLICANT: Phelps, Christopher Be
APPLICANT: Power, Christine
APPLICANT: Chvatchko, Yolande
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 43
APPLICANT: Chvatchko, Yolande
APPLICANT: Boschert, Ursula
TITLE OF INVENTION: Cytokine antagonist molecules
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-6
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PRIOR FILING DATE: 2003-04-30
PRIOR APPLICATION NUMBER: GB 0209884.6
PRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 43
SOFTWARE: SeqWin99, version 1.02
SEQ ID NO 6
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Best Local Similarity
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                                                                                                  CURRENT APPLICATION NUMBER: US/09/909,320
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
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APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/706,691
CURRENT FILING DATE: 2003-11-12
                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                   APPLICANT: Williams, P. Mickey
APPLICANT: Williams, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                              FILE REFERENCE: 10466-14
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                                                                 APPLICATION NUMBER: US 60/143,048 FILING DATE: 1999-07-07 APPLICATION NUMBER: US 60/145,698 FILING DATE: 1999-07-26
FILING
                  APPLICATION
                               APPLICATION NUMBER: US 60/146,222 FILING DATE: 1999-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 PISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
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D. US20020132240A1
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Kljavin, Iva.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Botstein, David
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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DATE:
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                                                                                                                                                                                                                                                                                                             Margaret Ann art, Timothy A.
                NUMBER: PCT/US99/20594
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1999-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 94;
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US-09-909-320-320
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PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 320
LENGTH: 450
                                                                                                                                                                                                                                                                                                                                          Matches
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es 72; Conserv
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
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FILING DATE: 1999-12-16
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APPLICATION NUMBER: PCT/US99/28565
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                                                                                 120 LSASQKIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAXQMLKNGRPVHT 179
180 SSTYSFSPONNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIY 226
                                       190 DSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVY
                                                                                                                           131 FTGEKTINLTVDVPISRPQVLV-ASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLN 189
                                                                                                                                                                     62 HTMPKYLLGSVNKSVVPDL--EYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGT
                                                                                                                                                                                                                                                                                                17 LAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYS--STSSDRPVVKWQLKR-
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Pred. No. 4.3e-17;
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                                                                                                                                                                                                                                                                                                                                                                                    Length 450;
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Gaps

119

61 73

RESULT 15 US-09-909-088B-320 GENERAL Sequence Patent No. US20020146709A1 APPLICANT: APPLICANT: Genentech, Inc. APPLICANT: Ashkenazi, Avi APPLICANT: Botstein, David APPLICANT: INFORMATION 320, Application US/09909088B Fong, Sherman Gao, Wei-Qiang Gerber, Hanspeter Gerritsen, Mary E. Goddard, A. Godowski, Paul J. Grimaldi, Christopher J. Eaton, Dan L. Ferrara, Napoleone Filvaroff, Ellen Hillan, Kenneth, J Gurney, Desnoyers, Austin L. Luc

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; SEQ ID NO 320
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-909-088B-320
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
HITLE OF INVENTION: Acids Encoding the Same
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OR FILING DATE: 1999-07-07
OR APPLICATION NUMBER: US 60/145,698
OR FILING DATE: 1999-07-26
OR APPLICATION NUMBER: US 60/146,222
OR FILING DATE: 1999-07-28
OR APPLICATION NUMBER: PCT/US99/20594
OR APPLICATION NUMBER: PCT/US99/20594
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FILING DATE: 1999-11-30
APPLICATION NUMBER: PCT/US99/28564
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FILING DATE: 2000-02-22
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                                                                                                     131 FTGEKTINLTVDVPISRPQVLV-ASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLN 189
                                                                        120 LSASQKİQVİVDDÞVTKÞVVQIHÞÞSGAVĖYVGNMTLTCHVÉGGTRLAYQMLKNGRÞVHT 179
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DSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVY 236
                                                                                                                                                                                                                                                           LKVFTTFLSFATGACSGLKVTVPSHTVHGVRGQALYLPVHYGFHTPASDIQII-WLFERP 61
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Mather, Jennie P.
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180 SSTYSFSPQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIY 226

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Search completed: July 26, 2005, 16:21:18 Job time: 62.4446 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

July 26, 2005, 15:58:02; Search time 13.8684 Seconds (without alignments) 1665.085 Million cell updates/sec Run on:

Title: Perfect score:

US-10-706-691-20 1205 1 MKRERGALSRASRALRLAPF.....NPISQGRSLPVKITVYRRSS 240

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:* Database :

pirl:* pir2:* pir3:* pir4:* 4 3 2 1. ..

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	biliary glycoprote.	biliary glycoprote	carcinoembryonic a	biliary glycoprote	biliary glycoprote	Ly-9.2 antigen - m	biliary glycoprote	biliary glycoprote	biliary glycoprote	pregnancy-specific	pregnancy-specific	neural cell adhesi	neural cell adhesi	junctional adhesio	C-CAM2a protein is	cell-adhesion mole	ecto-ATPase precur	biliary glycoprote	biliary glycoprote	neural cell adhesi	neural cell adhesi	nonspecific cross-	carcinoembryonic a	biliary glycoprote	biliary glycoprote	biliary glycoprote	transmembrane carc	biliary glycoprote	coxsackie- and ade
SUMMARIES	QI	JC1506	JC1512	A39037	JC1509	148268	A46500	S34338	JC1507	JC1511	A54879	176668	IJBONC	IJRTNC	S56749	S68177	823969	A44783	WMMSR1	JC1508	JE0100	JN0635	A27681	A35364	JH0395	JH0396	JH0394	C30127	A32164	JC7780
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neural cell adhesi	pregnancy-specific	pregnancy-specific	pregnancy-specific	pregnancy-specific	pregnancy-specific	pregnancy-specific	pregnancy-specific	pregnancy-specific	pregnancy-specific	pregnancy-specific	pregnancy-specific	pregnancy-specific	pregnancy-specific	pregnancy-specific	neural cell adhesi
IJHUNG	G43354	F43354	A43354	H43354	D43354	C43354	E43354	A28277	A33258	A31135	A35964	B33258	A35341	A27658	JE0099
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761	324	326	333	335	395	397	406	417	419	419	426	426	426	428	725
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		pecies: Mus musculus (house mouse)	ite: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text change 09-Jul-2004		Cuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
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	ary glycoprotein B - mouse	nlus (#sedn		nberg,
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RESULT

C.; Beauchemin, N. C; Spe C; Dat C; Acc R; McC

Gene 127, 173-183, 1993
A;Itle: Expression of the Bgp gene and characterization of mouse colon biliary glycopro A;Itle: Expression of the Bgp gene and characterization of mouse colon biliary glycopro A;Accession: JC1506
A;Accession: JC1506
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-278 <MCC>
A;Cross-references: UNIPROT: Q99232
C;Comment: This protein is expressed at the cell surface and plays a determinant role in

C;Genetics:

A Gener Bapb Superfamily: biliary glycoprotein; carcinoembryonic antigen precursor amino-terminal h. C. Superfamily: biliary glycoprotein; receptor C. Superfamily: biliary glycoprotein; receptor F. 1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology «CEAN» F. 159-216/Domain: immunoglobulin homology «IWM» F. 159-216/Domain: immunoglobulin homology «IWM» F. 199-104,153,195/Binding site: carbohydrate (Asn) (covalent) #status predicted

5. Gaps 6 Query Match 17.2%; Score 207.5; DB 2; Length 278; Best Local Similarity 32.1%; Pred. No. 9.3e-09; Matches 54; Conservative 32; Mismatches 73; Indels 9;

128 73 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITD g ઠ

129 DTF-TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPL 187 ò

셤

188 LNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITV 235 g ò

biliary glycoprotein H - mouse C,Species: Mus musculus (house mouse) C,Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004

C,Accession: JC1512
R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
R;McLuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
A;Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopro A;Reference number: JC1505; MUID:93273228; PMID:8500759
A;Accession: JC1512

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A; Accession: I48268
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Best Local &
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NiAlternate names: bliary glycoprotein homolog; calcium-dependent cell adhesion molecul
C;Species: Mus musculus (house mouse)
C;Date: 31-Uul-1991 #sequence_revision 31-Jul-1991 #text_change 09-Jul-2004
C;Accession: A39037; S13760

N;Turbide, C.; Rojas, M.; Stanners, C.P.; Beauchemin, N.
Biol. Chem. 266, 309-315, 1991
A;Title: A mouse carcinoembryonic antigen gene family member is a calcium-dependent cell
A;Reference number: A39037
A;Rocession: A39037

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                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 341;
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                                                                                                                                                                                                                                                                                                                                                                                                                   73; Indels
                                                                                                                                                                                                                                                                                                                                                         17.2%; Score 207.5; DB 2 32.1%; Pred. No. 1.2e-08; tive 32; Mismatches 73
                                                                                                                                                                                                                                                                                                                                                                                                                   54; Conservative
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A Jours 1919. Carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terminic (Superfamily). Carcinoembryonic antigen precursor amino-terminal proprotein; receptor antigen precursor amino-terminal homology cCEAN> Fi1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology cCEAN> Fi260-219/Domain: immunoglobulin homology cIMM1> Fi254-303/Domain: immunoglobulin homology cIMM2> Fi339-396/Domain: immunoglobulin homology cIMM3> Fi38-104,148,199,206,210,226,258,290,294,304,333,375/Binding site: carbohydrate (ABn) (cc
                                                                                                                                                                                                                                                                                                      A,Molecule type: mRNA
A,Residues: 1-458 <MCC>
A,Cross-references: UNIPROT:061351; GB:X67280
C,Comment: This protein is expressed at the cell surface and plays a determinant role in
C,Genetics:
A;Gene: BgpE
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R;Nedellec, P.; Dveksler, G.S.; Daniels, E.; Turbide, C.; Chow, B.; Basile, A.A.; Holmes, U. Virol. 68, 4525-4537, 1994
A;Title: Bgp2, a new member of the carcinoembryonic antigen-related gene family, encodes A;Reference number: A53995; MUID:94267915; PMID:8207827
                                                                                                                                                                                                               mouse colon biliary glycoprot
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C.Date: 24-Peb-1994 #sequence_revision 24-Peb-1994 #text_change 09-Jul-2004
C.Accession: JC1509
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                                                                                                                                Rimchaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N. Gene 127, 173-183, 1993
A;Title: Expression of the Bgp gene and characterization of mouse colon A;Reference number: JC1505; MUID:93273228; PMID:850759
A;Accession: JC1509
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15.2%; Score 183.5; DB 2,
Best Local Similarity 25.7%; Pred. No. 6.5e-07;
Matches 59; Conservative 41; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 15.4%; Score 186; DB 2; Local Similarity 27.8%; Pred. No. 8.2e-07; Ne 47; Conservative 35; Mismatches 79.
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C, Date: 02-Jul-1996 #sequence_revision
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Matches 47; Conserv
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A; Residues: 1-278 <MCC>
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c;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S34338
B;Huang, D.C.; Huang, X.F.; Novel, M.; Novel, G.
Submitted to the EMBL Data Library, July 1992
A;Boscription: A Clp-family gene present on the lactose-protease plasmid of lactococcus
A;Reference number: S34338
A;Retus: preliminary
A;Molecule type: mRNA
A;Retius: preliminary
A;Molecule type: mRNA
A;Reterences: UNIPROT:Q61352; EMBL:X67281; NID:g312585; PIDN:CAA47698.1; PID:g3125
B;McCualg, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
B;McLualg, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
B;McLualg, R.;McLualg,                                                                                                                                                                                                                                                                                                                                                                                             A46500
Ly-9.2 antigen - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A46500
R;Sandrin, M.S.; Gumley, T.P.; Henning, M.M.; Vaughan, H.A.; Gonez, L.J.; Trapani, J.A.;
J. Immunol. 149, 1636-1641, 1992
A;Fitle: Isolation and characterization of cDNA clones for mouse Ly-9.
A;Reference number: A46500; MUID:92373005; PMID:1506686
A;Accession: A46500
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Readus: L-629 <ASN>
A;Coss-references: GB:M8412; NID:g198931; PIDN:AAA39468.1; PID:g198932
A;Cross-references: C57BL/6
A;Roperimental source: C57BL/6
A;Note: sequence extracted from NCBI backbone (NCBIN:111651, NCBIP:111654)
C;Keywords: transmembrane protein
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A;Reference number: JC1505; MUID:93273228; PMID:8500759
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                                                               F----TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGK 185
                                                                                                             -----GPVHSGRETLYSNGSLLIQRVTMKDTGVYTIE--MTDQN 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 VVQSIGTEVIGTLRPDYRDRIRLFENG-SLLLSDLQLADEGTYEVEISITDDTFTGEKTI 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 PFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVT 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.2%; Score 183.5; DB 2 26.9%; Pred. No. 1.9e-06; cive 43; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 26.9
Matches 59; ~Conservative
TGTNKTIK-
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A;Residues: 1-81,'Q',83-141,'P',143-521 <MCC>
A;Cross-references: GB:X67281
A;Cross-references: GB:X67281
B;Williams, R.K.; Jiang, G.S.; Holmes, K.V.
Proc. Natl. Acad. Sci. U.S.A. 88, 533-536, 1991
A;Title: Receptor for mouse hepatitis virus is a member of the carcinoembryonic antigen is A;Reference number: A41093; WUID:91288498; PMID:1648219
A;Scatus: preliminary
A;Status: protein
A;Residues: protein
C;Comment: This protein is expressed at the cell surface and plays a determinant role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termine
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A;Reference number: JC1505; MUID:93273228; PMID:8500759
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C;Keywords: glycoprotein; receptor
C;FL-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;75-124/Domain: immunoglobulin homology <IMM1>
F;159-216/Domain: immunoglobulin homology <IMM2>
F;159-216/Domain: immunoglobulin homology <IMM2>
F;159-216/Domain: immunoglobulin comology <IMM2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Keywords: glycoprotein; receptor
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;16-0219/Domain: immunoglobulin homology <IMM1>
F;324-310/Domain: immunoglobulin homology <IMM2>
F;339-396/Domain: immunoglobulin homology <IMM3>
F;339-396/Domain: immunoglobulin homology <IMM3>
F;87,104,148,199,206,210,226,258,290,294,304,333,375/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DTF-TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNC-SHENGTKPSYTWLKDGKP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           biliary glycoprotein C - mouse
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
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R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
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31.7%; Pred. No. 1.4e-06;
tive 29; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 15.0%; Score 181; DB 2; Similarity 27.8%; Pred. No. 2.4e-06; 47; Conservative 34; Mismatches 80
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us-10-706-691-20.rpr

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neural cell adhesion molecule short domain form precursor - bovine
Mylternate names: NCAM-140
C;Alternate names: NCAM-140
C;Species: Bos primigenius taurus (cattle)
C;Date: 31.Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C;Accession: A29976; A38778; B44290; 805402
R;Lipkin, V.M.; Khramtsov, N.V.; Andreeva, S.G.; Moshnyakov, M.V.; Petukhova, G.V.; Rakit PEBS Lett. 254, 69-73, 1989
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A;Molecule type: mRNA
A;Residues: 1-475 <RES>
A;Cosectics: uniprof:Q62056; GB:M83344; NID:g200316; PIDN:AAA39916.1; PID:g200317
C;Cenetics:
A;Gene: CGM5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pregnancy-specific glycoprotein - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 17668
R;Rudert, F.; Saunders, A.M.; Thompson, J.A.; Rebstock, S.; Zimmermann, W.A.
A;Title: Characterization of murine carcinoembryonic antigen gene family members.
A;Reference number: 157007; MUID:92345715; PMID:1638085
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    83
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F;1-137/Domain: carcinoembryonic antigen precursor amino-terminal homology
F;399-456/Domain: immunoglobulin homology <1MM>
                                                           GTEVIGTLRPDYRDRIRLFENGSLILSDLQLADEGTYEVEISITDDTFTGEKTINLTVDV
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DPLEGVNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKW-----QLKRDKPVTVVQSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 TITRVLMEDDDLYSCMVENPISQGRSLPVKITV 235
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
C;Accession: A54879
R;Chan, H.; Chen, C.L.; Chou, J.Y.
Biochemistry 33, 9615-9626, 1994
A;Title: Characterization of two promoters of a rat pregnancy-specific glycoprotein gene
A;Reference number: A54879
A;Accession: A54879
A;Accession: A54879
A;Molecule type: DNA
A;Residues: 1-475 cCHE>
A;Crose-references: UNIRROT:Q62664; GB:U09815; NID:g497254; PIDN:AA56870.1; PID:g497255
A;Note: authors translated the codon GCT for residue 64 as Gly
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: glycoprotein
F;1-1378/Domain: carcinoembryonic antigen precursor amino-terminal homology cCEA1>
F;242-378/Domain: carcinoembryonic antigen precursor amino-terminal homology cCEA2>
F;399-456/Domain: immunoglobulin homology <IMM2>
                                                                                                                                                                                                                                                                                                                        Dilary glycoprotein G - mouse
C; Species: Mus musculus (house mouse)
C; Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C; Species: Mus musculus (house mouse)
C; Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C; Accession: JC1511
R; McCusiq, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
A; Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopro
A; Reference number: JC1505, MUID:93273228; PMID:8500759
A; Accession: JC1511
A; Molecule type: DNA
A; Residues: 1-341 cMCC>
A; Residues: 1-341 cMCC>
A; Residues: 1-341 cMCC>
A; Residues: 1-341 cMCC>
C; Goment: This protein is expressed at the cell surface and plays a determinant role in C; Genetics:
A; Genetics:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | : | : : | | : : | : | : : | | : : | : | : : | : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : : | : : : | : : : | : : : : | : : : : | : : : | : : : | : : : | : : : | : : : | : : : : | : : : : : | : : : : | : : : : | : : : : : : | : : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 STIVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 14.9%; Score 179.5; DB 2; Length 341; Best Local Similarity 31.7%; Pred. No. 1.8e-06; Matches 45; Conservative 29; Mismatches 63; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 LYSCMVENPISQGRSLPVKITV 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 EYQCEISNPVSVRRSNSIKLDI 232
                                                                                                             211 EYQCEISNPVSVRRSNSIKLDI 232
                                                           214 LYSCMVENPISQGRSLPVKITV 235
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A;Residues: 340-381 <>m2>
R;Small, S.O.; Haines, S.L.; Akeson, R.A.
R;Small, S.O.; Haines, S.L.; Akeson, R.A.
Neuron 1, 1007-1017, 1988
A;Title: Polypeptide variation in an N-CAM extracellular immunoglobulin-like fold is dev
A;Title: Polypeptide variation in an N-CAM extracellular immunoglobulin-like fold is dev
A;Reference number: I58136; MUID:90166485; PMID:2483093
A;Accession: I58136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: DNA
Residues: 355-364 ARES>
,Cross-references: GB:M32611; NID:g205643; PIDN:AAA41679.1; PID:g205644
;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu C;Superfamily: neural cell adhesion duplication; heparin binding; si. F;1-19/Domain: signal sequence #status predicted <51G>
F;1-19/Domain: signal sequence #status predicted <51G>
F;20-721/Domain: extracellular #status predicted <2KT>
F;20-721/Domain: immunoglobulin homology <IMM1>
F;32-91/Domain: immunoglobulin homology <IMM2>
F;122-156/Region: heparin binding #status predicted F;122-156/Region: heparin binding #status predicted F;208-29/Domain: immunoglobulin homology <IMM3>
F;208-29/Domain: immunoglobulin homology <IMM4>
F;208-29/Domain: imturacellular #status predicted <IMM7>
F;208-29/Domain: intracellular #status predicted <IMM7>
F;222,316,318-388,330-396,437-490/Disulfide bonds: #status predicted <IMM7>
F;222,316,318-348,434,460,4489/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                   A,Title: Expression of the unique NCAM VASE exon is independently regulated in distinct A,Reference number: A37795, MUID:91035620, PMID:1699951
                                                                                                                                                                                 A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 340-381 <SM2>
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Best Local Similarity 30.09
Matches 54; Conservative
                                                                                                                                                     A;Accession: B37795
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A; Residues: 20-36 < RQU>
A; Residues: 20-36 < RQU>
A; Residues: 20-36 < RQU>
A; Residues: 20-36 < RQU>
A; Residues: 20-36 < RQU>
A; Residues: 20-36 < RQU>
C; Comment: Various forms of NCAM are produced by alternative splicing.
C; Comment: Various forms of NCAM are produced by alternative splicing.
C; Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu C; Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si F; 1-19 foomain: signal sequence #status predicted < SIG.
F; 20-853/Product: neural cell adhesion molecule, short domain form #status experimental F; 120-19/Domain: immunoglobulin homology < IMML>
F; 132-191/Domain: immunoglobulin homology < IMMZ>
F; 151-156/Region: heparin binding #status predicted
F; 151-156/Region: heparin binding #status predicted
F; 122-286/Domain: immunoglobulin homology < IMM4>
F; 228-288/Domain: immunoglobulin homology < IMM4>
F; 221-396/Domain: intracellular #status predicted < IMM>
F; 720-731/Domain: intracellular #status predicted < IMM>
F; 720-731/Domain: intracellular #status predicted < IMM>
F; 738-853/Domain: intracellular #status predicted < IMM>
F; 738-853/Domain: intracellular #status predicted < IMM-
F; 738-853/Domain: intracellular #status predicted < IMM-
F; 738-853/Domain: intracellular #status predicted < IMM-
F; 738-853/Domain: intracellular #status predicted < IMM-
F; 738-853/Domain: intracellular #status predicted < IMM-
F; 738-853/Domain: intracellular #status predicted < IMM-
F; 738-853/Domain: intracellular #status predicted < IMM-
F; 778-773/NDM-P; 778-779/Domain: intracellular #status predicted < IMM-
F; 778-779/Pi / 
Title: Calmodulin-independent bovine brain adenylate cyclase. Amino acid sequence and Reference number: A32976; MUID:89378239; PMID:2776887 A32976
                                                                                                                                                                                                                                                                                                              Molecule type: protein
;Residues: 20-35;51-61;113-117;122-147;155-161;262-275;279-302;353-360;369-382;544-562;
;Note: the authors identified this protein as calmodulin-independent adenylate cyclase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;41-96,139-189,235-286,328-394,435-488/Disulfide bonds: #status predicted
F;222,314,346,432,458,487/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rougon, G.; Marshak, D.R.
Biol. Chem. 261, 3396-3401, 1986
Tittle: Structural and immunological characterization of the amino-terminal domain of Reference number: A44290; MUID:86140120; PMID:3512556
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N;Alternate names: NCAM-140
C;Specias: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S00846; B37795; I58136
R;Small, S.J.; Shull, G.E.; Santoni, M.J.; Akeson, R.
J. Cell Biol. 105, 2335-2345, 1987
A;Ticle: Identification of a cDNA clone that contains the complete coding sequence for A;Reference number: S00846; MUID:88059265; PMID:3680385
                                                                                                                                       ,Molecule type: mRNA
;Residues: 1-833 <LIP>
;Residues: 1-833 <LIP>
;Rocession: A38778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 EVEISITDDTFTGEKTINLTVDVP--ISRPQVLVASTTVLELSEAFTLNCSHENGTKPSY 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSLPPTIIWKHK------GRDVI--LKKDV--RFIVLTWNYLQIRGIKKTDEGTY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : | | | | : : | | : | | | | : | | SWIKDGEQIENEEDEKYLPSDDSSELTIRKVDKNDEAEYVCIAENKAGEQDASIHLKY 303
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30.9%; Pred. No. 5.4e-05;
tive 28; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 13.99
Best Local Similarity 30.9
Matches 55, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Accession: B44220,
A,Molecule type: pr
A,Note: 23-Glu was
C,Comment: NCAM med
C,Comment: Various
C,Superfamily: narious
C,Superfamily: also
F,1-19/Domain: sign
F,20-83/Produc: n
F,20-83/Produc: n
F,20-19/Domain: ex
F,34-98/Domain: imm
F,152-156/Region: h
F,152-156/Region: h
F,261-270/Region: h
F,261-270/Region: h
F,261-270/Region: h
F,261-270/Region: h
F,261-370/Region: h
F,261-370/Region: h
F,261-370/Region: h
F,261-370/Region: h
F,261-370/Region: h
F,361-370/Region: h
F,361-370/Domain: f
F,537-604/Domain: f
F,738-853/Domain: f
F,738-853/Domain: f
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C;Accession: A59406; S56749
R;Ozaki, H.; Ishli, K.; Horiuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamatsu, A.; Ki d. Immunol. 163, 553-557, 1999
A;Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistribution A;Reference number: A59406; MUID:99323940; PMID:10395639
A;Accession: A59406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               junctional adhesion molecule precursor - human N;Alternate names: F11 platelet antigen; platelet adhesion molecule PAM-1; platelet C;Species: Homo sapiens (man) C;Date: 27-0ct-1995 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                        245
                                                                                                                                                                                                                                                                                                                                                233
                                                                                                                    120
                                                                                                                                                                         187
                                                                                                                                                                                                                               121 EVEISITDDTFTGEKTINLTVDVP--ISRPQVLVASTTVLELSEAFTLNCSHENGTKPSY 178
                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q9Y624; GB:AAD42050; NID:g5326797; PIDN:AAD42050.1
                                                                                                                                                                                                                                                                   TWLKDGKPLLN----DSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPI-SQGRSLPVKI
                                                                                                                    61 SSDRPVVXWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY
                                                                                                                                                  Gaps
                                                              24;
                                                           74; Indels
13.8%; Score 166; DB 1;
30.0%; Pred. No. 6.5e-05;
tive 28; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-299 <OZA>
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A;Wolecule type: mRNA A;Residues: 1-858 <SMA> Cross-references: UNIPROT:P13596; EMBL:X06564 R;Small, S.J.; Akeson, R.

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C-CAMAa protein isoform precursor - rat
C.CAMAa protein isoform precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Baccession: S68177
R;Lucka, L.; Cichocka, I.; Baeumler, K.; Bechler, K.; Reutter, W.
Bur. J. Biochem. 234, 527-535, 1955
A;Title: A short isoform of carcinoembryonic-antigen-related rat liver cell-cell adhesic
A;Reference number: S68177; MUID:96128184; PMID:8536699
A;Reference number: S68177; MUID:96128184; PMID:8536699
A;Retus: preliminary
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R; Naik, U.P.; Ehrlich, Y.H.; Kornecki, E. Biochem. J. 310, 155-162, 1995

Biochem. J. 310, 155-162, 1995

A; Title: Mechanisms of platelet activation by a stimulatory antibody: cross-linking of a A; Reference number: S56749; MUID:95374438; PMID:7646439

A; Rocession: S56749

A; Rolecule type: protein

A; Rolecule type: protein

A; Residues: 28-49, 'X',51-53,62-73,'E',75-103,123,'F',125-130;'FDKDXIIVLNXY';'LT',206,'X'

A; Note: the order of the peptides other than the amino terminus was not determined C; Genetics:
A; Rolecule and A; A; Constant all sequence #status predicted <SIG>
F; L-25/Domain: signal sequence #status predicted <SIG>
F; C-299/Product: junctional adhesion molecule #status predicted <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 NCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQG 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                343 TCFSKD-TGVSVRWLFNSQSLQLTDRMTLSQDNSTLRIDPIKREDAGDYQCEISNPVSFR 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 VVKWQLKRDKPVTVVQSIGTEVI---GTLRPDYRDRIRLFENGSLLLSDLQLADEGTYEV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 EISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPS-YTWL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 MVSEEGGNSYGEVKVKLIVLVPPSKPTVNIPSSAT--IGNRAVLTCSEQDGSPPSEYTWF 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GTKAQVERKL-LCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSS--P 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 GALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSSTSSDRP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 13.7%; Score 165.5; DB 2; Length 299; l Similarity 26.2%; Pred. No. 1.8e-05; 60; Conservative 31; Mismatches 111; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDGIVMPTNPKSTRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARN 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 KDGKPL-----LNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVEN 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 458;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227 RSLPVKITV 235
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ISHPIKLDV 410
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Best Local Similarity
Matches 42; Conserv
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Sequence 119, App	Sequence 119, App	Sequence 119, App	Sequence 1, Appli	Sequence 22, Appl	Sequence 22, Appl	Sequence 67, Appl	Sequence 6, Appli	Sequence 6, Appli	Sequence 26, Appl	Sequence 16, Appl	Sequence 6, Appli	Sequence 20, Appl	Sequence 10, Appl	Sequence 12, Appl	Sequence 2, Appli	Sequence 18, Appl	Sequence 8, Appli
US-09-909-064-119	US-09-905-381A-119	US-09-906-618-119	US-09-953-499-1	US-08-597-495B-22	US-09-068-051A-22	US-09-336-536-67	US-09-254-465A-6	US-09-953-499-6	US-08-928-383B-26	US-09-877-730-16	US-09-877-730-6	US-09-877-730-20	US-09-877-730-10	US-09-877-730-12	US-09-877-730-2	US-09-877-730-18	US-09-877-730-8
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28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William, I.
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
PILE REFERENCE: 10466-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 2001-07-17

PRIOR APPLICATION NUMBER: PCT/USO/04414

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR PILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26

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PRIOR FILING DATE: 1999-07-28

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APPLICATION NUMBER: PCT/US99/20944
FILING DATE: 1999-09-13
PPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
Sequence 320, Application US/09907794A Patent No. 6635468 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                  Godowski, Paul J.
Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
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Paoni, Nicholas F.
                                                                                                                                                                                                                                                                 Gerber, Hanspeter
Gerritsen, Mary E.
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Mather, Jennie P.
                                                                     Genentech, Inc.
Ashkenazi, Avi
Botstein, David
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Eaton, Dan L.
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Sao, Wei-Qiang
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RESULT 3
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31.7%; Pred. No. 1.4e-19;
tive 43; Mismatches 102; Indels
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Paoni, Nicholas F.
Roy, Margaret Ann
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Gerritsen, Mary E.
Goddard, A.
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
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Best Local Similarity 31.74
Matches 72; Conservative
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CORGANISM: Homo Sapien
US-09-907-794A-320
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CURRENT APPLICATION NUMBER: US/09/902,775A

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: DCT/USO0/0414

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-29

PRIOR PILING DATE: 1999-11-20

PRIOR PILING DATE: 1999-11-20

PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-11-30

PRIOR PILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-03

PRIOR PILING DATE: 1999-13-03

PRIOR PILING DATE: 1999-13-03

Sequence 320, Application US/09902775A
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Wood, William, I.
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Stewart, Timothy A.
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Filvaroff, Ellen
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Paoni, Nicholas F.
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Gerber, Hanspeter
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Mather, Jennie P.
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ORGANISM: Homo Sapien
US-09-902-775A-320
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62 HTMPKYLLGSVNKSVVPDL--EYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGT 119
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                                                                                                                                     3 LKVFTTFLSFATGACSGLKVTVPSHTVHGVRGQALYLPVHYGFHTPASDIQII-WLFERP
                                                                                                   17 LAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYS--STSSDRPVVKWQLKR-
                                                    Gaps
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     Length 450;
                                                 Indels
23.4%; Score 282; DB 4; Le
31.7%; Pred. No. 1.4e-19;
tive 43; Mismatches 102;
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TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/USO/0414
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-18
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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Hillan, Kenneth, J
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Paoni, Nicholas F.
Roy, Margaret Ann
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Mather, Jennie P.
Query Match
Best Local Similarity 31.74
Matches 72; Conservative
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AFFLICANII: "WOOD, WILLIAGH, 1.

AFFLICANII: "WOOD, WILLIAGH, 1.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: GNE-1618P2C12

CURRENT APPLICATION NUMBER: US/09/903,603A

CURRENT FILING DATE: 2001-00-11

PRIOR PILING DATE: 2000-00-22

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR PILING DATE: 1999-09-08

PRIOR PILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR PILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LKVFTTFLSFATGACSGLKVTVPSHTVHGVRGQALYLPVHYGFHTPASDIQII-WLFERP 61
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Best Local Similarity 31.7%; Pred. No. 1.4e-19;
Matches 72; Conservative 43; Mismatches 102; Indels
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PRIOR FILING DATE: 1999-12-16
PRIOR PELING DATE: 1999-12-16
PRIOR PELING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30910
PRIOR PELING DATE: 1999-12-20
PRIOR PELING DATE: 1999-12-20
PRIOR PELING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
LENGTH: 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
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PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
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US-09-904-920A-320
; Sequence 320, Application US/09904920A
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US-09-903-603A-320
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PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
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PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
PRIOR PILING DATE: 423
PRIOR PILING DATE: 423
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Patent No. 6767995
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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Mather, Jennie P.
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Botstein, David
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Eaton, Dan L.
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US-09-906-700-320
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Best Local Similarity
Matches 72; Conserva
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US-09-903-603A-320
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ATTLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14

FILE REFERENCE: 10466-14

CURRENT PILING DATE: 2001-07-18

PRIOR PILING DATE: 2001-07-22

PRIOR PILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR PILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-07-36

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                                                                                                                                                              17 LAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYS--STSSDRPVVKWQLKR-
; Score 282; DB 4; Length 450;
; Pred. No. 1.4e-19;
43; Mismatches 102; Indels 10;
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PRIOR APPLICATION NUMBER: PCT/US99/21090
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PRIOR FILING DATE: 1999-09-15
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Grimaldi, Christopher
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerber, Hanspeter
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Mather, Jennie P.
Query Match
Best Local Similarity 31.7*
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: William, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TILLE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/904,920A

CURRENT PILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-08

PRIOR FILING DATE: 1999-07-08

PRIOR FILING DATE: 1999-07-08

PRIOR FILING DATE: 1999-07-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-18

PRIOR APPLICATION NUMBER: PCT/US99/2094

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-11-29

PRIOR FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-03

PRIOR FILING DATE: 1999-12-03

PRIOR FILING DATE: 1999-12-03

PRIOR FILING DATE: 19
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Pan, James
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Filvaroff, Ellen
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Eaton, Dan L.
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CORGANISM: Homo Sapien
US-09-904-920A-320
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APPLICATION NUMBER: PCT/US99/23089

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 450;
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31.7%; Pred. No. 1.4e-19;
iive 43; Mismatches 102; Indels
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PELING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/3099
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
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PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1099-12-20
PRIOR PLING DATE: 2000-01-05
PUMBER OF SEQ ID NOS: 423
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Patent No. 6818746
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hangpeter
Gerriteen, Mary E.
Goddard, A.
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Stewart, Timothy A.
Tumas, Daniel
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Paoni, Nicholas F.
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Botstein, David
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Eaton, Dan L.
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Best Local Similarity
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US-09-909-064-320
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US-09-905-381A-320
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APPLICANT: Williams, P. Mickey
BPPLICANT: Wood, William, I.
IILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IILE OF INVENTION: Acids Encoding the Same
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PRIOR APPLICATION NUMBER: PCT/US00/04114
PRIOR FILING DATE: 2000-02-22
PRIOR PILING DATE: 1990-07-07
PRIOR PILING DATE: 1990-07-07
PRIOR PILING DATE: 1990-07-08
PRIOR PILING DATE: 1990-07-28
PRIOR PILING DATE: 1990-09-08
PRIOR PILING DATE: 1990-09-08
PRIOR PILING DATE: 1990-09-08
PRIOR PILING DATE: 1990-09-08
PRIOR PILING DATE: 1990-09-13
PRIOR PILING DATE: 1990-09-13
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CURRENT APPLICATION NUMBER: US/09/906,618
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Grimaldi, Christopher J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Ferrara, Napoleone
Filvaroff, Ellen
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Gerritsen, Mary E
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Mather, Jennie P.
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ORGANISM: Homo Sapien
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Sequence 5729, Application US/09513999C

Sequence 5729, Application US/09513999C

SEQUENCE 5729, Application US/09513999C

GENERAL INFORMATION:

APPLICANT: Ducaert, A.

APPLICANT: Duclert, A.

TITLE OF INTENTION: Expressed Sequence Tags and Encoded Human Proteins.

PAPELICANT: Giordano, J.Y.

TITLE OF INTENTION: Expressed Sequence Tags and Encoded Human Proteins.

PAPELICANT: Giordano, J.Y.

FILE REPERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm

SEQ ID NO 5729
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                                                                                                                   3 LKVFTTFLSFATGACSGLKVTVPSHTVHGVRGQALYLPVHYGFHTPASDIQII-WLFERP
                                                                                                                                                                     74 -DKPVTVVQSIGTEVIGTLRPDYRDRIRLF-ENGSLLLSDLQLADEGTYEVEISIT-DDT
                                                                      17 LAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYS--STSSDRPVVKWQLKR-
                         Gaps
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                         10;
                                                                                                                                                                                                                                                                                                                                                                                           180 SSTYSFSPQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIY 226
                                                                                                                                                                                                                                                                                                                                                               190 DSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVY 236
                         Indels
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Best Local Similarity 31.7%; Pred. No. 1.4e-19; Matches 72; Conservative 43; Mismatches 102;
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Patent No. 669968
GENERAL INFORMATION:
APPLICANT: Kornecki, Elizabeth
APPLICANT: Schocka, Malgorzata B.
TITLE OF INVENTION: Human Platelet F11 Receptor
FILE REFERENCE: 011.0021
CURRENT FILING DATE: 1999-09-16
PRIOR FILING DATE: 1999-09-16
PRIOR PILING DATE: 1999-09-16
PRIOR FILING DATE: 1998-09-16
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
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Best Local Similarity 100.0%; Pred. No. 8.7e-21;
Matches 58; Conservative 0; Mismatches 0;
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; ORGANISM: Homo sapiens
US-09-513-999C-5729
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ORGANISM: Homo sapiens
US-09-397-243D-13
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-0-0-08
PRIOR FILING DATE: 2000-0-0-08
PRIOR FILING DATE: 2000-0-0-08
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PRIOR FILING DATE: SO00-0-0-08
PRIOR FILING DATE: SO00-0-0-0-08
PRIOR FILING DATE: PASSEQ FOR WINDOWS VERSION 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 VVQSIGTEVIGTLRPDYRDRIR-LFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTI 137
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                                                                                                                                                                                                                                                                                      KPVTVVQSIGTEVI-GTLRPDYRDRIRLFEN-----GSLLLSDLQLADEGTYEVEISITD 128
                                                                                                                                                                                                                                                                                                                                                                                                                                DTFTGEKT-INLTVDVPISRPQVLVASTTVLELSEAFTLNC-SHENGTKPSYTWLKDGKP 186
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                                                                                                                                                                                            7 WILLLCLÓTWP-EAAGKDSEIFTVNGILGESVTFPVNIQEPROVK-IIAWTSKTSVAYVT 64
                                                                                                                                                16 RLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQY-SSTSSDRPVVKWQLKRD 74
                                                                                   Gaps
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       14.1%; Score 170; DB 4; Length 316; 24.8%; Pred. No. 1.2e-08; ive 46; Mismatches 110; Indels
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Patent No. 6812339
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US-09-149-476-483
US-09-149-6-483, Application US/09149476
; Sequent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
Query Match
Best Local Similarity 24.81
Matches 58; Conservative
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Best Local Similarity 26.1
Matchés 55, Conservative
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US-09-949-016-6428
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CORRENT FILING DATE: 1998-09-08
EARLIER FILING DATE: 1998-09-08
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,615
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,500
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,612
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EARLIER APPLICATION WUMBER: 60/043,569
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,311
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/040,336
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,163
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,583
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,581
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-04-11
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FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
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LICATION NUMBER: 60/043,671
ING DATE: 1997-04-11
                  FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/643,674
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,669
                                                                                              FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,312
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APPLICATION NUMBER: 60/043,672
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APPLICATION NUMBER: 60/056,889
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LING DATE: 1997-08-22
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G DATE: 1997-08-22
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FILING DATE: 1997-08-22
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CATION NUMBER: 60/056,888
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LING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,874
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NLQIYRRIGKPKITQSLMASVNSTCNVTLTCSVEKEEKNVTYNW----SPLGEEGNVLQI 180 65 PGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRY 124 79 VVQSIGTEVIGTLRPDYRDRIR-LFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTI 137 NLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTK-PSYTWLKDGKPLLNDSRML-- 194 20 FVYLLLIQIDPLEGVNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKP-VT Query Match 13.9%; Score 167.5; DB 4; Length 329; Best Local Similarity 26.1%; Pred. No. 2.2e-08; Matches 55; Conservative 40; Mismatches 93; Indels 23 -LSPDOKVLTITRVLMEDDDLYSCMVENPIS 224 APPLICATION NUMBER: 60/047,589 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,593 APPLICATION NUMBER: 60/047,614 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,578 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/056,632 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,908 EARLIER FILING DATE: 1997-06-13 EARLIER APPLICATION NUMBER: 60/061,060 EARLIER FILING DATE: 1997-10-02 APPLICATION NUMBER: 60/047,501 APPLICATION NUMBER: 60/056,664 APPLICATION NUMBER: 60/056,876 APPLICATION NUMBER: 60/056,909 APPLICATION NUMBER: 60/056,875 APPLICATION NUMBER: 60/056,862 APPLICATION NUMBER: 60/057,669 FILING DATE: 1997-09-05 APPLICATION NUMBER: 60/056,881 APPLICATION NUMBER: 60/056,887 FILING DATE: 1997-05-23 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 FILING DATE: 1997-05-23 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 1997-06-06 FILING DATE: 1997-04-11 FILING DATE: 1997-08-2 FILING DATE: 1997-08-2 FILING DATE: 1997-08-2 APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1997-00 FOTPEDQELT FILING DATE: 138 125 181 195 g 원 ઠે g ò ò 셤 à

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FACELL NO. SEL2AS.

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FILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFRENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

FRICK APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFFWARE: FASESEQ FOR WINDOWS VERSION 4.0

ENDITY: 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 PGDSETAPVVTVTHRNYYERIHALGPNYNLVISDLRMEDAGDYKADINTQADPYTTTKRY 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 NLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTK-PSYTWLKDGKPLLNDSRML-- 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 FVYLLLIQIDPLEGVNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKP-VT 78
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APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
TILLE OF INVENTION: Compositions Isolated From Skin Cells
TILLE OF INVENTION: Compositions Isolated From Skin Cells
TILLE OF INVENTION: LORDO: 1010.1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOUTHARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.9%; Score 167.5; DB 4; Length 3 Best Local Similarity 26.1%; Pred. No. 2.2e-08; Matches 55; Conservative 40; Mismatches 93; Indels
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|----YTCTAQNPVS 204
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Sequence 7327, Application US/09949016
Patent No. 6812339
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NAME/KEY: UNSURE:

LOCATION: (247)...(247):

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LOCATION: (289)...(289)

US-09-188-930-189
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; ORGANISM: Human
US-09-949-016-7327
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US-09-188-930-189
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66 VVKWQLKRDKPVTVVQSIGTEVI---GTLRPDYRDRIRLFENGSLLLSDLQLADEGTYEV 122
                                                                                                                                                                                         59 RVEWKFD------GGDTTRLVCYNNKITASYEDRVTFLPTG-ITFKSVTREDTGTYTC 109
                                                                                                                                                                                                                                 123 EISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPS-YTWL 181
                                                                                                   2 GTKAQVERKL-LCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSS--P 58
                                                                             6 GALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSSTSSDRP
                                     Indels 27; Gaps
                                                                                                                                                                                                                                                                                                                                     182 KDGKPL-----LNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVEN 221
 Length 299;
Query Match 13.7%; Score 165.5; DB 3; Best Local Similarity 26.2%; Pred. No. 3e-08; Matches 60; Conservative 31; Mismatches 111;
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Search completed: July 26, 2005, 16:15:53 Job time : 18.7207 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

July 26, 2005, 15:57:23; Search time 98.0554 Seconds (without alignments) 2000.159 Million cell updates/sec Run on:

US-10-706-691-26 1962 1 VNITSPVRLIHGTVGKSALL.....TAGVHIIREQDEAGFVEISA 383 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 1612378 segs, 512079187 residues Searched:

1612378

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:* Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	, Description	O8n7i3 homo sapien	homo	แนย ก	4 home	5 homo	omou o	9 cerco	P06729 homo sapien	Q6sz58 macaca assa	Q6sz62 papio anubi	m	Q6sz56 macaca neme	Q6sz57 macaca arct	Q61354 mus musculu	Q68z61 macaca fasc	Q6sz60 macaca mula	Q6uy47 homo sapien	mus m	Q96jal homo sapien	mus m	Q86xk7 homo sapien	homo	Q99795 homo sapien	Q8wmv3 bos taurus	P70193 mus musculu	O95791 homo sapien	P97268 cavia porce	Q61353 mus musculu	6 homo	homo	m aum
SUMMAKIES	ID	O8N7I3	Q671P8	Q640R3	Q6ZWL4	Q8ND35	Q6UX10	068259	CD2 HUMAN	068258	Q6SZ62	Q6SZ63	Q6SZ56	Q6SZ57	061354	Q6SZ61	092890	Q6UY47	099232	LIG1_HUMAN	Q613 <u>4</u> 9	Q86XK7	Q6MZS4	A33 HUMAN	QBWMV3	LIG1 MOUSE	095791	P97268	061353	075296	701960	QBRINS
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de	Query Match	99.8	8.66	94.3	67.2	43.6	13.7	11.4		•			10.8	ö	10.8			10.5	•	•	•	٠	٠	7.6	٠		•	•	9.5	•		4.6
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Q9r067 rattus norv	Q9r066 rattus norv	P78310 homo sapien	Q91w66 mus musculu	P97792 mus musculu	Q9dbj8 mus musculu	Q9ukv4 homo sapien	Q9cva4 mus musculu	Q9jhl7 rattus norv	Q61351 mus musculu	Q61352 mus musculu	Q6van5 bos taurus	Q6van6 bos taurus	Q6van7 bos taurus
Q9R067	Q9R066	CXAR HUMAN	Q91W66	CXAR MOUSE	Q9DBJ8	Q9UKV4	Q9CVA4	Q9JHL7	061351	061352	Q6VAN5	Q6VAN6	Q6VAN7
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ALIGNMENTS

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Y; PRT; 416 AA 22, Created) 22, Last sequence upd 26, Last annotation u L02530. cordata; Craniata; Verte imates; Catarrhini; Hom W. Worinaga M., Kawamura Y., Worinaga M., Kawamura D. H., Nishikawa T., Su ugano S.; D. He EMBL/GenBank/DDBJ 11 3-1ike. 1. IKE; 1. 11 994 MW; 47120CA9A00EE1	ore 1958; ed. No. 3.3 Mismatches	DRPV 	EISI EISI	DGKPL DGKPL	TILS	ERKN	RSPA
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Carralboror From N.T.

Statesberg R.L., Falmoold B.A., Grouse L.H., Derge J.G.,

Ratausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Ratausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Ratausperg R.L., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Ratschul S.F., Jordan H., Moore T., Max S.L., Wang J., Heich F.,

Raph B., Bonaten M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,

Rank S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rank S.S., Worley K.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Rathards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Rathards S., Worley K.D., Sodergren B.J., Lu X., Gibbs R.A.,

Rathards S., Worley A.C., Shevchenko Y., Bouffard G.G.,

Raphey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rathards R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rathards R.W., Rataka U., Smailus D.E., Schnerch A., Schein J.E.,

Ray Jones S.J., Marra M.A.;

Ray and mouse CDNA sequences.",

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          329 TIEPGPPGYSVSPPVPGRSPGLPIRSARRYPRSPARSPAGRTHTSPPRAPSSPGRSRSS 388
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                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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STRAIN=CS7BL/6; TISSUE=Brain;
Director MGC Project;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC082537; AAH82537.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      413 AA; 45665 MW; B6EFCA2D6D2CA3C1 CRC64;
               25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
2900042201Rik protein (Fragment)
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                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                              NCBI_TaxID=10090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 LYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACWKPSKRKQKKL 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKQNSLEYMDQNDDRLKPEADTLPRSGEQERKNPMALYILKDKDSPETEENPAPEPRSAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                274 EKQNSLEYMDRNDDRLKPEADTLPRSGEQERKNPWALYILKOKDSPETEENPAPEPRSAT 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPGPPGYSVSPAVPGRSPGLPIRSARRYPRSPARSPATGRTHSSPPRAPSSPGRSRSASR 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 EPGPPGYSVSPAVPGRSPGLPIRSARRYPRSPARSPATGRTHSSPPRAPSSPGRSRASR 393
STIVLELSEAFILNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
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                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shen S., Moh M.C.;
"A gene related to human hepatocellular carcinoma.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY047587; AAQ93018.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 416 AA; 46055 MW; 7B8882298BEB4ABF CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          394 TLRTAGVHIIREQDEAGPVEISA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLRTAGVHIIREQDEAGPVEISA 383
                                                                                         TLRTAGVHIIREODEAGEVEISA 416
                                                                TLRTAGVHIIREQDEAGPVEISA 383
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SMART; SM00409; IG; 2.
SMART; SM00408; IGc2; 1.
PROSITE; PS50835; IG_LIKE; 1.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
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                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
Homo sapiens (Human).
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    PRELIMINARY;
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                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
CORDITAXID=9606;
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                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                        367 AA
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InterPro; IPR003399; Ig.
InterPro; IPR00110; Ig-like.
InterPro; IPR003598; Ig_c2.
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389 SRSLRTAGVQRIREQDESGQVEISA 413
                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein FLJ16002.
Homo sapiens (Human).
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -218 FLLVTLVTVCACWKPSKRKQKKLEKQNSLEYMDQNDDRLKPEADTLPRSGEQERKNPMAL
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bioinformatics assessment.";
EMBL, AX358345; AAQ88711.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
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                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL834419; CAD39081.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 165 AA; 18161 MW; 5052FA978C437486 CRC64;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
10-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypotherical protein DKFZp5470159 (Fragment).
Name=DKFZp5470159;
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Last annotation update)
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SMART; SM00409; IG; 3
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185 MVENPISQGRSLPVKITVYRRSSLYIILS-TGGIFLLVTLVTVCACWKPSKRKQKKLEKQ 243
 --- PGPPGYSVS----- PAVPG-----RSPGLPIRSARRYPRSPARSPATGRIHSS 344
 P06729; Q967E5;
01-JAN-1988 (Rel. 06, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
T-cell surface antigen CD2 precursor (T-cell surface antigen T11/Leu-
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 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
 SEQUENCE FROM N.A., AND VARIANT HIS-266.
Hall R.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
[8]
 Proc. Natl. Acad. Sci. U.S.A. 83:8718-8722(1986).
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 351
 PRT;
 EMBO J. 7:1675-1682(1988).
 STANDARD;
 Homo sapiens (Human)
 NCBI_TaxID=9606;
 antigen.";
 REVISIONS
 HUMAN
 242
 302
 Name=CD2;
 CD2_HUMAN
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 68 LFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLEL 127
 128 SEAFTINCSHENGTKPSYTWLKDGKPLINDSRMLLSPDQKVLT---ITRVLMEDDDLYSC 184
 57 TLRPDYRDRIRLF-ENGSLLLSDLQLADEGTYEVEISIT-DDTFTGEKTINLTVDVPISR 114
 POVLV-ASTIVLELSEAFTINCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDOKVLTITR 173
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 Damschrouger M.M., Kozhich A.A., Woods R.M., Cheng L., Mullikin B.A., Wilson S.D., Ulbrandt N.D., Bachy C.M., Wu H., Suzich J.A., Kiener B.A., Dall'Acqua W.F., White W.I.;

Riener P.A., Dall'Acqua W.F., White W.I.;

"Analysis of human and primate CD2 molecules by protein sequence and epitope mapping with anti-human CD2 antibodies.";

Mol. Immunol. 41:985-1000(2004).

HSSP; P08921; 1A64.

GO; GO:001621; Cintegral to membrane; IEA.

GO; GO:001621; Cintegral to membrane; IEA.

InterPro; IRR007110; Ig-like.
 Gaps
 Gaps
 Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey). Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi; mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercocebus.
 99
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 Query Match 11.4%; Score 224; DB 2; Length 358 Best Local Similarity 23.5%; Pred. No. 2.5e-05; Matches 84; Conservative 61; Mismatches 146; Indels
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H-InvDB; HIX0000931; --
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 88
MEDINE-2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
REAUSDERE Pancreas, and Spleen;
REDINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RETAUSDERS R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,
A Lotchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Scholer M.J., Usdin T.B., Toshiyuki S., Carnino F., Frange C.,
A Eronstein M.J., Usdin T.B., Toshiyuki S., Carnino F., Prange C.,
A Robards S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Willialon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Williadon D.K., Muzny D.M., Green E.D., Dickson M.C.,
A Blakesley R.W., Touchman M., Madan A., Rodrigues S., Sanchez A.,
A Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
A Schnerch A., Schehu J.B., Jones S.J.M., Marra M.A.;
A Schnerch A., Schehu J.B., Jones S.J.M., Marra M.A.;
A Generation and initial analysis of more than 15,000 full-length human mouse cDNA sequences.",
A Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 MEDLINE=92311658; PubMed=1377404;
Hahn W.C., Menu B., Bothwell A.L.M., Sims P.J., Bierer B.E.;
Hahn W.C., Menu B., Bothwell A.L.M., Sims P.J., Bierer B.E.;
Hoverlapping but nonidentical binding sites on CD2 for CD58 and a second ligand CD59.";
Science 256:1805-1807(1992).
-!- FUNCTION: CD2 interacts with lymphocyte function-associated antigen (LFA-3) and CD48/BCM1 to mediate adhesion between T cells and other cell types. CD2 is implicated in the triggerring of T-cells, the cytoplasmic domain is implicated in the signaling function.
 STRUCTURE BY NMR OF 25-129.
MEDLINE=94348865; PubMed=7915183; DOI=10.1016/0969-2126(93)90009-6;
Withka J.M., Wyss D.F., Wagner G., Arulanandam A.R.N., Reinherz E.L.,
 "Structure of the glycosylated adhesion domain of human T lymphocyte
 MEDLINE=95381065, PubMed=7544493, Wyss D.F., Choi J.S., Li J., Knoppers M.H., Willis K.J., Arulanandam A.R., Smolyar A., Reinherz E.L., Wagner G., "Conformation and function of the N-linked glycan in the adhesion
 X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 25-206.
MEDLINE=95086863; PubMed=7994575;
Bodian D.L., Jones B.Y., Harlos K., Stuart D.I., Davis S.J.;
"Crystal structure of the extracellular region of the human cell adhesion molecule CD2 at 2.5-A resolution.";
Structure 2:755-766(1994).
 SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
DATABASE: NAME=PROW, NOTE=CD guide CD2 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd2.htm".
 cell
 MEDLINE=88039075; PubMed=2444890; DOI=10.1038/329842a0;
Peterson A., Seed B.;
"Monoclonal antibody and ligand binding sites of the T erythrocyte receptor (CD2).";
 SUBUNIT: Interacts with CD2AP (By similarity).
 Science 269:1273-1278(1995).
 STRUCTURE BY NMR OF 25-129
 Nature 329:842-846(1987).
 Structure 1:69-81(1993).
 domain of human CD2.
 CD59-BINDING DATA.
 glycoprotein CD2
 Recny M.A.;
 MUTAGENESIS.
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the European Bioinformatics Institute. There are no restrictions on its
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@18b-sib.ch).
 11;
 .; NAS.
 By similarity.
By similarity.
By similarity.
N-linked (GlCNAC. .) (Potential).
N-linked (GlCNAC. .) (Potential).
N-linked (GlCNAC. .) (Potential).
O - H (in dbSNP:699738).
/FTId=VAR 017104.
K->R: Loss of LFA-3 binding.
Q->K: Loss of LFA-3 and CD59 binding.
Y->D: Loss of LFA-3 and CD59 binding.
 Gaps
 GO; GO:0005515; F:protein binding; MAS.
GO; GO:0005515; F:protein binding; MAS.
GO; GO:000166; P:protein binding; MAS.
GO; GO:000166; P:cell surface receptor linked signal transdu...
GO; GO:0001637; P:cell-cell adhesion; MAS.
GO; GO:0001766; P:lpjid raft polarization; TAS.
GO; GO:0001766; P:lpjid raft polarization; TAS.
GO; GO:0001010; P:nadural killer cell activation; MAS.
GO; GO:0001010; P:requlation of T-cell differentiation; NAS.
GO; GO:004510; P:T-cell activation; TAS.
InterPro; IPR00424; CD2.
 61;
 Length 351;
 T-cell surface antigen CD2.

Extracellular (Potential).

Cytoplasmic (Potential).

Ig-like V-type.
Ig-like C2-type.
Ig-like C2-type.
IrA-3 (CD58) binding region 1.

IFA-3 (CD58) binding region 2.
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3D-structure; Antigen; Cell adhesion; Glycoprotein;
Immunoglobulin domain; Polymorphism; Repeat; Signal; T-cell;
 Indels
 . 186990; -.
GO:0005887; C:integral to plasma membrane; NAS.
 11.2%; Score 219.5; DB 1; 23.6%; Pred. No. 4.6e-05; tive 53; Mismatches 148;
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EMBL, M16336, AAA35571.1; --
EMBL, M19366, AAA53095.1; --
EMBL, M1978, AAA53095.1; --
EMBL, M1978, AAA53095.1; JOINED.
EMBL, M19800, AAA53095.1; JOINED.
EMBL, M19804, AAA53095.1; JOINED.
EMBL, X07871, CAA30721.1; JOINED.
EMBL, X07872, CAA30721.1; JOINED.
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 AL135798; CAC14840.1;
BC033583; AAH33583.1;
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IGYA; NMR; @=25-129.
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 Similarity
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 246 LEYMDQNDDRLKPEADTLPRSGEQERKNPMALYILKDKDSPETEENPAPEPRSATE---- 301
 :||:|| || ::|
----QRNDBELEIRAH---RVAIBERGRKPHQIPASTPQNPAASQHPPPPPPPGHRSQAPSH 295
 35 GALGQDIDLDIPSFQMSDDIDDIKWEKTSDK------KKIAQFRKEKETFEEKDAY
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Last annotation update)
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 Cluster of differentiation 2 (Fragment)
 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
 PRELIMINARY;
 344 AA;
 SEQUENCE FROM N.A. Pubmed=15302161;
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 LSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMV 186
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 Damschroll I. M. Kozhich A.A., Woods R.M., Cheng L., Mullikin B.A., Wille Backy C.M., Wu H., Suzich J.A., Wille Backy C.M., Wu H., Suzich J.A., Wilenson S.D., Ulbrandt N.D., Backy C.M., Wu H., Suzich J.A., Kiener P.A., Dall'Acqua W.E., White W.I.; "Analysis of human and primate CD2 molecules by protein sequence and epitope mapping with anti-human CD2 antibodies."; Mol. Immunol. 41:985-1000 (2004).

Mol. Immunol. 41:985-1000 (2004).

HSSP; PO8921; 1A64.

GO; GO:001621; Cintegral to membrane; IEA.

GO; GO:001755; P:cell adhesion; IEA.

InterPro; IPR00110; Ig-like.
 Gaps
 Macaca assamensis (Assam's macaque) (Assam's monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Cercopithecinae; Macaca.
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75 KLFKNGTLKIKHLKIHDQDSYKVSIYDTKGKNVLEKTFDLKIQERVSEPKI---SWTCIN 131
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A Dameschroder W.M., Kozhich A.A., Woods R.M., Cheng L., Mullikin B.A., A Dameschroder W.M., Kozhich A.A., Woods R.M., Cheng L., Mullikin B.A., A Wilson S.D., Ulbrandt N.D., Bachy C.M., Wu H., Suzich J.A., Kiener P.A., Dall'Acqua W.F., White W.I.;
T "Analysis of human and primate CD2 molecules by protein sequence and primape company with anti-human CD2 antibodies.";
Mol. Immunol. 41:985-1000 (2004).
R EMBL; AY445041; AAR15888.1; -.
R HSSP; P08921; 1A64.
R GO; GO:0016021; C:integral to membrane; IEA.
R GO; GO:0016021; C:integral to membrane; IEA.
R GO; GO:0016021; C:integral to membrane; IEA.
R InterPro; IPR009124; CD2.
R InterPro; IPR00110; Ig-1ike.
R Pfam; PF05790; C2-8et; 1.
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Damschroder M.M., Kozhich A.A., Woods R.M., Cheng L., Mullikin B.A.,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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SEQUENCE
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 Name=CD2;
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 RLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLE 126
 127 LSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMV 186
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"Analysis of human and primate CD2 molecules by protein sequence and epitope mapping with anti-human CD2 antibodies.";
MOI. Immunol. 41:985-1000(2004).
HSSP: P08921: 1A64.
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InterPro; IPR007110; Ig-like.
Pfam; PP05790; C2-set; 1.
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 Pan troglodytes (Chimpanzee)
 Local Similarity 23.3
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 NCBI_TaxID=9598;
 302
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 186 CTAGNKVSKESRMETVSCPEKGLDIYLIIGICGGGSLLMVFVALLVFYITKRKKQRS--- 242
 67 RLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLE 126
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X MEDLINE=93273228; PubMed=8500759; DOI=10.1016/0378-1119(93)90716-G;
A McCuaig K., Rosenberg M., Turbide C., Beauchemin N., Nedellec P.;
A McCuaig K., Rosenberg M., Turbide C., Beauchemin N., Nedellec P.;
T "Expression of the Bgp gene and characterization of mouse colon
T biliary glycoprotein isoforms.";
Gene 127.173-183(1993).
R EMBL; X67283; CAA4700.1; -.
R PIR; JC1512; JC1512.
R HSSP; GG1353; IL62.
R MGD; MG1:1347245; Ceacaml.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR0031598; Ig_c2.
R Pfam; PF00047; ig; I.
R Pfam; PF00047; ig; I.
Wilson S.D., Ulbrandt N.D., Bachy C.M., Wu H., Suzich J.A., Kiener P.A., Dall'Acqua W.F., White W.I.; "Analysis of human and primate CD2 molecules by protein sequence and epitope mapping with anti-human CD2 molecules by protein sequence and epitope mapping with anti-human CD2 antibodies."; Mol. Immunol. 41:985-1000(2004).

EMBL; AY445040; AAR1S887.1; -. HSSP; P08921; 1A64.
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Biliary glycoprotein precursor.
Name=Ceacaml; Synonyms=Bgph;
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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 DB 2; Length 341;
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 293 РЅНКРІРРСНКУОНОРОККРРАРЅСТОVНООКСРРІРКРКУОРКРР 338
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InterPro; IPR007110; Ig-like.
Pfam; PF05790; C2-set; 1.
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 Damschroder M.M., Kozhich A.A., Woods R.M., Cheng L., Mullikin B.A., Wilson S.D., Ulbrandt N.D., Bachy C.M., Wu H., Suzich J.A., Kiener P.A., Dall'Acqua W.F., White W.I.;

"Analysis of human and primate CD2 molecules by protein sequence and epitope mapping with anti-human CD2 molecules by protein sequence and epitope mapping with anti-human CD2 molecules by sprotein sequence and molecules of human and primate CD2 molecules by protein sequence and epitope mapping with anti-human CD2 molecules by protein sequence and molecule mapping with anti-human CD2 molecules by protein sequence and epitope mapping with anti-human CD2 molecules by protein sequence and epitope mapping with anti-human CD2 molecules by protein sequence and epitope mapping with anti-human CD2 molecules by protein sequence and epitope mapping with anti-human CD2 molecules by protein sequence and epitope mapping with anti-human CD2 molecules by protein sequence and epitope mapping with anti-human CD2 molecules by protein sequence and epitope mapping with anti-human CD2 molecules by protein sequence and epitope mapping with anti-human CD2 molecules by protein sequence and epitope mapping with anti-human CD2 molecules by protein sequence and epitope mapping with anti-human CD2 molecules by protein sequence and epitope mapping with anti-human CD2 molecules by protein anti-human CD2 molecules by protein sequence and epitope mapping with anti-human CD2 molecules by protein anti-human CD2 molecules by protein anti-human CD2 molecules by protein anti-human CD2 molecules by protein anti-human CD2 molecules by protein anti-human CD2 molecules by protein anti-human CD2 molecules by protein anti-human CD2 molecules by protein anti-human CD2 molecules by protein anti-human CD2 molecules by protein anti-human CD2 molecules by protein anti-human CD2 molecules by protein anti-human CD2 molecules by protein anti-human CD2 molecules by protein anti-human CD2 molecules by protein anti-human CD2 molecules by protein anti-human CD2 molecules by protein anti-human CD2
 67; Gaps
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 Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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OM protein - protein search, using sw model

July 26, 2005, 15:57:23; Search time 61.4446 Seconds (without alignments) 2000.159 Million cell updates/sec Run on:

US-10-706-691-20 1205 1 MKRERGALSRASRALRLAPF.....NPISOGRSLPVKITVYRRSS 240 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### STIMMARTES

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| 7      | 202.5  |       | 341    |    | Q61354    | enm a              |
| 8      | 193.5  |       | 292    |    | Q6UY47    | homo               |
| 6      | 189.5  | 15.7  | 235    |    | 075296    | homod              |
| 10     |        | 15.2  | 272    |    | Q8R1N5    | แนยก               |
| 11     |        | 15.2  | 340    |    | Q61349    | Q61349 mus musculu |
| 12     | 183.5  | 15.2  | 538    | ~  | Q8C9E4    | BUM                |
| 13     | 183.5  |       | 645    |    | Q6NZB6    | Qenzbe mus musculu |
| 14     | 183.5  |       | 649    |    | Q7TMP7    | Q7tmp7 mus musculu |
| 15     | 183.5  | 15.2  | 654    |    | LY9_MOUSE | Q01965 mus musculu |
| 16     | 182    | ٠.    | 471    |    | Q9DAV5    | mus                |
| 17     | 181    | 15.0  | 458    |    | 061351    | mus                |
| 18     | 181    | 15.0  | 521    |    | 061352    | Q61352 mus musculu |
| 19     | 178.5  | 14.8  | 475    |    | Q62664    | ratt               |
| 20     | 177.5  | 14.7  | 278    |    | Q61350    | mus                |
| 21     | 177.5  | 14.7  | 341    |    | Q61353    | mus                |
| 22     | 174.5  | 14.5  | 471    |    | Q9D2U0    | Q9d2u0 mus musculu |
| 23     | 173.5  | 14.4  | 365    |    | Q6VANS    | Q6van5 bos taurus  |
| 24     | .173.5 | 14.4  | 372    |    | Q6VAN6    | Q6van6 bos taurus  |
| 25     | 173.5  | 14.4  | 429    |    | Q6VAN7    | Q6van7 bos taurus  |
| 26     | 173.5  | 14.4  | 436    |    | Q6VAN8    | Q6van8 bos taurus  |
| 27     | 173.5  | 14.4  | 475    |    | Q810J1    | ET I               |
| 28     | 173.5  | 14.4  | 520    |    | Q925P2    | 2 mus              |
| 29     |        | 14.3  | 7      | ~  | P70161    | enm 1              |
| 30     | 170.5  | 14.1  | 234    | ~  | Q78T27    | Q78t27 mus musculu |
| 31     | ^      | 14.1  | 0      | 7  | Q9JHY1    | Q9jhyl rattus norv |

|                  | Q6rwt5 bos taurus<br>Q6rwt6 bos taurus |                  |        |                  |        |        |        |       | homo    |
|------------------|----------------------------------------|------------------|--------|------------------|--------|--------|--------|-------|---------|
| Qerwt3<br>Qerwt4 | Qerwis<br>Qerwig                       | Q9NX42<br>O95791 | 096107 | Q62056<br>Q9JHL7 | Q9R038 | O9UIB6 | Q9UIB7 | 09260 | Q6 FHA8 |
| 0 0              | 04                                     | 00               | ~      | ~ ~              | N      | ~      | ~      | 7     | 0       |
| 368<br>375       | 432<br>439                             | 284<br>325       | 327    | 475<br>448       | 476    | 241    | 272    | 280   | 328     |
|                  |                                        |                  |        |                  |        |        |        |       |         |
| 14.1<br>14.1     | 14.1<br>14.1                           | 14.0             | 14.0   | 13.9             | 13.9   | 13.9   | 13.9   | 13.9  | 13.9    |
|                  | 170 14.1<br>170 14.1                   |                  | -      |                  | _      | _      | _      | _     |         |

# ALIGNMENTS

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Receptor.
 SEQUENCE
 Query Match
 0640R3;
 Q640R3
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 61 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY 120
 LKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSS 240
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 181 LKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSS 240
 9
 Suzuki O., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Shiohata N., Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y., Matsumura Y., Moriya S., Chiba E., Momiyama H., Onogawa S., Kataoka E., Momiyama H., Onogawa S., Kataoka R., Kuga N., Kuroda A., Satoh I., Kamata K., Takahashi E., Kataoka R., Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Magatsuma M., Murakawa K., Satoo K., Magano S., Naghirama A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Naghari K., Masuho Y., Nagai K., Isogai T.; Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
 1 MERERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST
 1 MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQXSST
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ö
 99.7%; Score 1201; DB 2; Length 416; llarity 99.6%; Pred. No. 1.6e-84; Conservative 1; Mismatches 0; Indels (
 A Shen S., whoh M.C.;

"A gene related to human hepatocellular carcinoma.";

"A gene related to human hepatocellular carcinoma.";

"Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY047587; AAQ3018.1; -.

R InterPro; IPR007599; IG-1ike.

R InterPro; IPR007599; IG-2.

R Pfam; PF00047; ig; I.

R SMART; SM00409; IG; 2.

R SMART; SM00409; IG; 2.

R PROSTER; PSS0839; IG_LIKE; 1.
 Hypothetical protein.
SEQUENCE 416 AA; 46055 MW; 7B8882298BEB4ABF CRC64;
 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ16002.
Homo sapiens (Human).
 Created)
Last sequence update)
Last annotation update)
 367 AA
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25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
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 Hypothetical protein.
 al Similarity
239; Conserv
 SEQUENCE FROM N.A.
TISSUE=Brain;
 SEQUENCE FROM N.A.
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 NCBI_TaxID=9606;
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 61
 Query Match
 Local
 Q6ZWL4
 Matches
 RESULT 3
OGENMLA
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SA Straubberg R.L., Feingold B.A., Groue L.H., Shenmen C.M., Schuler G.D.,

A Itschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Itschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzatne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Marxy D.M., Sodergren B.J., Lu X., Gibbs R.A.,

A Nillalon D.K., Marxy D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Redriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Nores S.J., Marra M.A.;

Jones A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.;

T "Generation and initial analysis of more than 15,000 full-length human

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 ö
 240
 180
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 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDSRDRIRLFENGSLLLSDLQLADEGTY
 121 EVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTW
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 413 AA
EMBL; AK122595; BAC85486.1; -. GO; GO:0004872; F:receptor activity; IEA. InterPro; IPR003599; IG. InterPro; IPR00110; Ig-like. InterPro; IPR00110; Ig-like. InterPro; IPR001598; Ig_c2. Ffam; PF00047; Ig; 1. SMART; SM00409; IG; 2. SMART; SM00409; IGc2; 1. PROSITE; PS50835; IG_LIKE; 1.
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STRAIN=C57BL/6; TISSUE=Brain;
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Matches 238; Conservative
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 Mus musculus (Mouse)
 Name=2900042E01R1k;
 SEQUENCE FROM N.A.
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-DKPVTVVQSIGTEVIGTLRPDYRDRIRLF-ENGSLLLSDLQLADEGTYEVEISIT-DDT 130
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 131 FIGEKTINLTVDVPISRPQVLV-ASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLN
 69 KGNPVSTNAEIVHFVIGTNKTTIGPAHSGRETVYSNGSLLIQRVTVKDIGVYIIE--MID
 73 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITD
 129 DTF-TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPL
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SEQUENCE FROM N.A.

MEDLINE=91093141, PubMed=1985902;

Turbide C., Rojas M., Stanners C.P., Beauchemin N.;

Turbide C., Rojas M., Stanners C.P., Beauchemin N.;

"A mouse carcinoembryonic antigen gene family member is a calcium—dependent cell adheaton molecule.";

J. Biol. Chem. 266:309-315(1991).

EMBL; X53084; CAA37251.1; -.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Best Local Similarity 32.1%; Pred. No. 1.3e-07;
Matches 54; Conservative 31; Mismatches 74; Indels 9;
 188 LNDSRMLLSPDOKVLTITRVLMEDDDLYSCMVENPISOGRSLPVKITV 235
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 190 DSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVY 236
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 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Carcinoembryonic antigen family member protein precursor.
 34 Potential.
278 Potential.
29943 MW; 1A9CEBF18770258C CRC64;
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Last sequence update)
Last annotation update)
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 341 AA.
 (TrEMBLrel. 01, Created)
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MGD, MGI:1347245, Ceacaml.
InterPro, IPR007110, Ig-like.
InterPro, IPR003598; Ig_c2.
 Pfam; PF00047; ig; 1.
SMART; SM00408; IGc2; 1.
PROSITE; PS50835; IG_LIKE; 1.
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(TrEMBLrel. 2
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 PRELIMINARY;
 34
 PIR; A39037; A39037.
PIR; JC1506; JC1506.
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35 2
278 AA;
 Mus musculus (Mouse)
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01-NOV-1996 (
01-OCT-2003 (
 01-NOV-1996
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Q99232
ID Q99232
 061354;
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 Signal
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 VVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTYEVBIS 120
 126 ITDDTFTGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGK 185
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 MEDLINE=22897296; PubMed=12975309; DOI=10.1101/gr.1293003; MEDLINE=22897296; PubMed=12975309; DOI=10.1101/gr.1293003; MEDLINE=22897296; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Kimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshaqiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard.A., Wood W.I.,
 Gaps
 17 LAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYS--STSSDRPVVKWQLKR-
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 PILINDSRMILSPDQKVLITITRVLMEDDDLYSCVVENPISQVRSLPVKITVYRRSS 235
 "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins:
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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 10;
 Length 413;
 Length 450;
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 Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC008237; AAH82537.1; -.
NON TER 1
 SEQUENCE 413 AA; 45665 MW; B6EFCA2D6D2CA3C1 CRC64;
 PROSITE; PS50835; IG LIKE; 2.
SEQUENCE 450 AA; 50114 MW; A22FF822CC3CB226 CRC64;
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Last annotation update)
 Score 1146; DB 2;
Pred. No. 2.8e-80;
3; Mismatches 3;
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 450
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 PRT;
 Dioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
EMBL; A7358345; AAQ88711.1; -.
InterPro; IPR003599; IG.
InterPro; IPR007110; IG-like.
InterPro; IPR003598; Ig-22.
Pfam; PF00047; ig: 1.
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Best Local Similarity 97.4%;
Matches 229; Conservative
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Director MGC Project,
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 Query Match
Best Local Similarity
----- 72; Conserva
 ORFNames=UNQ305;
 NCBI_TaxID=9606;
 Q6UXI0;
05-JUL-2004
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AAQ88451.1;
 NCBI TaxID=9606;
 EMBL; AY358084;
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 Query Match
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 73 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITD 128
 129 DTF-TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPL 187
 : | | : | | : | | : : | 194
127 ENFRTEATVQFHVHQPVTQPSLQVTNTVKEL-DSVTLTCL-SNDIGANIQWLFNSQSL 184
 MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Klim, H.S., Klimowski L., Jin Y., Johnson S., Lee J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P.;
 "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."; Secreted and transmembrane proteins: a Genome Res. 13:2265-2270(2003).
 Gabs
 SECURALE, TUSTUS-COLON;
MEDLINE-93273228; PubMed=8500759; DOI=10.1016/0378-1119(93)90716-G;
MEDLINE-93273228; PubMed=8500759; DOI=10.1016/0378-1119(93)90716-G;
MCUaig K., Rosenberg M., Turbide C., Beauchemin N., Nedellec P.;
"Expression of the Bgp gene and characterization of mouse colon biliary glycoprotein isoforms.";
Gene 127:173-183(1993).
EMBL; X67283; CAA47700.1; -.
PIR; JC1512; JC1512.
MGD; MGI:1347245; Ceacaml.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig-C.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
 Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
 9
 16.8%; Score 202.5; DB 2; Length 341; 32.1%; Pred. No. 1.7e-07; tive 31; Mismatches 74; Indels 9;
 185 QLTERMTLSQNNSILRIDPIKREDAGEYQCEISNPVSVKRSNSIKLDI 232
 188 INDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITV 235
 341 AA; 36901 MW; B5278D6606996341 CRC64;
 Last sequence update)
Last annotation update)
 Potential
 Created)
 Biliary glycoprotein precursor.
Name=Ceacaml; Synonyms=Bgph;
Mus musculus (Mouse).
 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
 Pfam, PF00047; ig; 1.
SMART; SM00408; IGc2; 1.
PROSITE; PS50835; IG_LIKE; 1.
 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, CEACAM3.
 54; Conservative
 PRELIMINARY;
 Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 ORFNames=UNQ3098;
 NCBI_TaxID=9606;
 SEQUENCE
 Query Match
Best Local S
 Signal.
 Q6UY47:
 Matches
 RESULT 8

OGUY47

ID QGUY47

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TVVQSIGTEVIGT-LR---PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTG 133
 133 QASHHLRVYESVAQPSIQASSTTVTE-KGSVVLTC-HTNNTGTSFQWIFNNQRLQVTKRM 190
 78 TVVQSIGTEVIGT-LR---PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTG 133
 134 EKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRM 193
 73
 30 APTTAWLFIASAPFEVAE-----GENVHLSVVYLPEN----LYSYGWYKGKTV 73
 Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S., Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S., Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S., Abna H., Velasco N., Do L., Regala W., Terry A., Garnes J., Danganan L., Poundstene P., Christensen M., Amico-Keller G., Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G., Liu S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.; submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.

R KSSP, Q61353; 1L6Z.

R HSSP, Q61353; 1L6Z.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR0073598; Ig-2.
 30 APTTAWLFIASAPFEVAE-----GENVHLSVVYLPEN----LYSYGWYKGKTV
 18 APFVYLLLIQIDPLEGVNIISPVRLIHGTVGKSALLSVQYSSISSDRPVVKWQLKRDKPV
 18 APFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPV
 23; Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 23;
 Length 235;
 Length 292;
 Indels
 194 LLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITV 235
 InterPro; IPR003599; IG.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR007110; Ig-2.
Pfam; PF00047; Ig; 1.
SWART; SW00409; IG; 2.
SWART; SW00409; IGc2; 1.
PROSITE; PS06385; IG LIKE; 1.
SROUNCE 292 AA; 32315 MW; 2D4DE7851E301C57 CRC64;
 191 KLSWFNHVLTIDPIRQEDAGEYQCEVSNPVSSNRSDPLKLTV
 Created)
Last sequence update)
Last annotation update)
 / Match 15.7%; Score 189.5; DB 2; Local Similarity 29.3%; Pred. No. 1.1e-06; Ne 65; Conservative 35; Mismatches 99;
 Match 16.1%; Score 193.5; DB 2; Local Similarity 29.7%; Pred. No. 6.8e-07; les 66; Conservative 34; Mismatches 99;
 ..
 235 AA
 PRT;
 01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-OCT-2003 (TrEMBLrel. 25,
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=
 PRELIMINARY;
 R29124 1.
Homo sapiens (Human)
 SEQUENCE FROM N.A.
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70

Gaps

39;

---- OYSSTSSDRPVVKWQ

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71 LKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDT 130
 84 TGTNKTIK------GPVHSGRETLYSNGSLLIQRVTMKDTGVYTIE--MTDQN 128
 131 F----TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGK 185
 STRAIN=BALB/C; TISSUE=Kidney;
MEDLINE=94267915; PubMed=8207827;
Nedellec P., Dveksler G.S., Daniels E., Turbide C., Chow B.,
Nadellec P., A.A., Holmes K.V., Beauchemin N.;
"Bgp2, a new member of the carcinoembryonic antigen-related gene
"Bgp2, a new member of the carcinoembryonic antigen-related gene
family, encodes an alternative receptor for mouse hepatitis viruses.";
 24 LLASWSPPTTAQVTVMAFPLHAAEGNNVILVVYNMMKGVSAFSWHKGSTTSTNAEIVRFV
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 186 PLINDSRMLLSPDOKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITV 235
 15.2%; Score 183.5; DB 2; Length 272; 25.7%; Pred. No. 3.7e-06; Live 41; Mismatches 91; Indels 39;
 STRAIN=BALB/c; TISSUE=Kidney;
Robitaille J., Izzi L., Daniels E., Zelus B., Holmes K.V.,
Beauchemin N.;
 Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF101164; AAC99458.1; -.
HSSP; Q61353; 1L6Z.
HGG1.1347246; Ceacam2.
GO; GO:0009986; C:cell surface; IDA.
InterPro; IPR007110; Ig-like.
 Pfam; PF00047; 1g; 1. SMART; SMO048; 1Gc2; 1. SMART; SMO0408; 1Gc2; 1. SPECSITE; PS50835; 1G LIKE; 1. SEQUENCE 340 AA; 37506 MW; 99BP5A02C2C2AASE CRC64;
 biliary glycoprotein.
27C18C401781C37D CRC64;
 01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Biliary glycoprotein 2 long isoform.
Name=Ceacam2; Synonyms=Bgp2;
Mus musculus (Mouse).
 15.2%; Score 183.5; DB 2;
Llarity 25.7%; Pred. No. 4.9e-06;
Conservative 41; Mismatches 91;
 24 LLIQTDPLEGVNITSPVRLIHGTVGKSALLSV----
 24 LLIQTDPLEGVNITSPVRLIHGTVGKSALLSV----
 Potential
 Created)
 PRT;
 1 34 Po
35 272 Do
272 AA; 29983 MW;
 J. Virol. 68:4525-4537(1994).
 PROSITE, PS50835; IG LIKE; 1.
 (TrEMBLrel. 01,
 59; Conservative
 PRELIMINARY;
 SM00408; IGc2; 1
 Query Match
Best Local Similarity
Matches 59; Conserv
 Similarity
 SEQUENCE FROM N.A
 SEQUENCE FROM N.A
 NCBI_TaxID=10090;
 Q61349;
01-NOV-1996
 CHAIN
SEQUENCE
 Query Match
 Local
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SIGNAL
SMART;
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 SEQUENCE FROM N.A.

STRAIN=FVBLN; TISSUE=Kidney;

MEDLINE=2238825; PubMed=1247932; DOI=10.1073/pnas.242603899;

MEDLINE=2238825; PubMed=1247932; DOI=10.1073/pnas.242603899;

MISCANI S.P., Zebeberg B.A., Grouse L.H., Derge J.G.,

Altschul S.P., Zebeberg B., Buetow K.H., Schaefer C.F., Bhar N.R.,

Hopkins R.F., Jozdan H., Moore T., Max S.I., Wang J., Hsieh F.,

Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M., Soares M.B., Bonaldo M.F., Casrainci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

M. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Pahey J., Helton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

M. Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
EPNQLIAAYVIDTHVRTPGPAYSGRETISPSGDLHFQNVTLEDTGYYTLQVTYRNSQIE- 132
 EKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRM
 Nedellec P., Dveksler G., Daniels E., Turbide C., Chow B., Basile A., HOLMES K.V., Beauchemin N.;
"Bgp2, a new member of the carcinoembryonic antigen related gene family, encodes an alternative receptor for the mouse hepatitis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
CEA-related cell adhesion molecule 2 (Biliary glycoprotein
 Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 LLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITV 235
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
 A
 Viruses, ", Virol. 68:4525-4537(1994).
EMBL; BCC024320; AAH24320.1; -.
EMBL; X76085; CAA53699.1; -.
PIR; 148268; 148268.
HSSP; QG1353; 116Z.
MGD; MGI:1347246; Ceacam2.
GO; GO:0009986; C:cell surface; IDA.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
 (TrEMBLrel. 21, Created)
 PRT;
 STRAIN-BALB/c; TISSUE-Colorectal; MEDLINE-94267915; PubMed-8207827;
 precursor).
Name=Ceacam2; Synonyms=Bgp2;
 SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Kidney;
 and mouse cDNA sequences.
 PRELIMINARY;
 Pfam; PF00047; ig; 1.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 Strausberg R.
 -JUN-2002
74
 134
 194
 QBRINS;
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70

Gaps

39;

Indels

Length 340;

--- QYSSTSSDRPVVKWQ

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 71 LKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDT 130
 84 TGTNKTIK-------GPVHSGRETLYSNGSLLIQRVTMKDTGVYTIE--MTDQN 128
 P----TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGK 185
24 LLASWSPPTTAQVTVMAFPLHAAEGNNVILVVYNMMKGVSAFSWHKGSTTSTNAEIVRFV 83
 the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
 MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA lbraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
 STRAIN=CS7BL/6J; TISSUE=Thymus; MEDLINE=9927953; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 3 days neonate thymus CDNA, RIERA full-length enriched
library, clone:A630078M16 product:lymphocyte antigen 9, full insert
 STRAIN=CS7BL/GJ; TISSUE=Thymus;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itch M., Sumin N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muzamatsu M., Inoue Y., Kira A., Hayabhizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
 186 PLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITV 235
 SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Thymus;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 538 AA.
 Created)
 PRT;
 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
The FANTOM Consortium,
 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Thymus;
 (TrEMBLrel. 23,
 RIKEN FANTOM Consortium;
 PRELIMINARY;
 sequence. (Fragment).
 Mus musculus (Mouse)
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 01-MAR-2003
 Name=Ly9;
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34 EIEHII-WNC---PPKALALVFYKKDITILDKGYNGRLKVSEDGYSLYMSNLTKSDSGSY 129
 EVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLEL-SEAFTLNCSHENGTKPS-- 177
 14 GPLSENPRMSQQQIFSPILWIPLLFILMGLGASGKETPPTVISGMLGGSVTFSLNISKDA 73
 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=CSTBL/6J; TISSUB=Thymus;
A Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
A Rukuda S., Furuno M., Harameto K., Hiracka T., Hirozane T.,
Hayashida K., Hayatsu N., Hirameto K., Hiracka T., Hirozane T.,
Hayashida K., Hayatsu N., Hirameto K., Hiracka T., Hirozane T.,
A Ratch H., Kawai J., Kojima Y., Konno B., Konno H., Kouda M., Koya S.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
A Tagawa A., Takhashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (UIL-2001) to the EMBL/GenBank/DDBJ databases.
 Σ.
 6 GALS---RASRALRLAPFVYL-LLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSSTS
 SDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENG-SLLLSDLQLADEGTY
 YTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKI 233
 |:| :: | :: | |:| | ||:| | ||:| | ||:| | ||:| | ||:| | ||:| | ||:| | ||:| | ||:| | ||:| | ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| |
 :
 STRAIN.CSTBL/6NCT: TISSUE-Hematopoietic Stem Cell;
MEDLINE-22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;
MEDLINE-22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold R.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 DB 2; Length 538;
 Indels
sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771 (2000).
 60040 MW; 7DC7FB9C64BFE9A6 CRC64;
 Last sequence update)
Last annotation update)
 15.2%; Score 183.5; DB 2; 27.1%; Pred, No. 8.6e-06;
 MGD; MGI:96885; Ly9.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
InterPro; IPR003599; Ig-11ke.
 Created)
 EMBL; AK042288; BAC31215.1; -
 LIKE; 2.
 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
 Local Similarity 27.19
nes 64; Conservative
 PRELIMINARY;
 Ly9 protein (Fragment).
 PROBLE; 13; 1.
SMART; SMO0409; IG; 2.
PROSITE; PS50835; IG L.
NON TER 538 538
 Mus musculus (Mouse)
 538 AA;
 [1]
SEQUENCE FROM N.A.
 1HNG
 NCBI_TaxID=10090;
 P08921;
 05-JUL-2004
05-JUL-2004
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 SEQUENCE
 Query Match
 Q6NZB6;
 Q6NZB6
 HSSP;
 Best Loc
Matches
 RESULT 13
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Query Match
 Local
 Matches
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 121 HAQINQKNVILTTNKEFTLHIYEKLQKPQIIVESVTPSDTDSCTFTLICT-VKGTKDSVQ 179
 EVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLEL-SEAFTLNCSHENGTKPS-- 177
 64
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., Mallahy S.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Paleton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
 5 GPLSENPRMSQQQIFSPILWIPLLFILMGLGASGKETPPTVISGWLGGSVTFSLNISKDA
 65 EIEHII-WNC---PPKALALVFYKKDITILDKGYNGRLKVSEDGYSLYMSNLTKSDSGSY
 6 GALS---RASRALRLAPFVYL-LLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSSTS
 62 SDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENG-SLLLSDLQLADEGTY
 178 YTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKI 233
 STRAIN=CS7BL/6NCr; TISSUE=Hematopoietic Stem Cell; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
 19;
 DB 2; Length 645;
 15.2%; Score 183.5; DB 2; Length 27.1%; Pred. No. 1.1e-05; ive 45; Mismatches 108; Indels
 Strausberg R.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases
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Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
 EMBL; BC066212; AAH66212.1; -. GO; GO:0005615; C:extracellular space; TAS. GO; GO:0016021; C:integral to membrane; TAS. InterPro; IPR003599; Ig.
 649 AA
 PRT;
 PROSITE; PS50835; IG_LIKE; 2.
 (TrEMBLrel. 25, (TrEMBLrel. 26, I
 64; Conservative
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Name=Ly9;
 Pfam; PF00047; ig; 1.
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 Mus musculus (Mouse)
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 SEQUENCE FROM N.A.
 01-MAR-2004
 01-OCT-2003
 01-OCT-2003
 SEQUENCE
 Query Match
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.E., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Rahas S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McKaran P.J., McKeram K.J., Malek J.A., Gunarathe P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villaton D.K., Mixny D.M., Sodergren E.J., Lu X., Gibs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.,
Jones S.J., Marra M.A.,
Tand mouse cDNA sequences.";
 124
 177
 :|: : | | | | | : | | | : | | | | 183
 68
 61
 9 GPLSENPRMSQQQIFSPILWIPLLFLLMGLGASGKETPPTVISGMLGGSVTFSLNISKDA
 6 GALS---RASRALRLAPFVYL-LLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSSTS
 62 SDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENG-SLLLSDLQLADEGTY
 121 EVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLEL-SEAFTLNCSHENGTKPS--
 |:| :: | :: | |:| | ||:| | ||:| | ||:| | ||:| | ||:| | ||:| | ||:| | ||:| | ||:| | ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:
 178 YTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKI 233
 Gaps
 6
 Name=Ly9; Synonyms=Ly-9;
Nam smusculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 LY9 MOUSE STANDARD; PRT; 654 AA.

Q01965, Q9ES29; Q9ES35; Q9ES36;
01-JUN-1994 (Rel. 29, Created)
28-FEE-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
T-lymphocyte surface antigen Ly-9 precursor (Lymphocyte antigen (Cell-surface molecule Ly-9).
 19;
 SEQUENCE FROM N.A., AND POLYMORPHISM.
STRAIN=129/Sv. BALB/C, and CS/BL/6; TISSUE=Spleen;
MEDLINE=20424510; PubMed=10970093; DOI=10.1007/s002510000209;
TOVAL V., de la Evente M.A., Pizcueta P., Bosch J., Engel P.;
 Length 649;
 Indels
 Strausberg R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
 SEQÜENCE 649 AA; 72414 MW; AD6A09381C063B34 CRC64;
 SEQUENCE FROM N.A. STRAIN=CS7BL/6NCr; TISSUE=Hematopoietic Stem Cell;
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
 15.2%; Score 183.5; DB 2; 27.1%; Pred. No. 1.1e-05; rative 45; Mismatches 108;
 EMBL; BC055380; AAH55380.1; -...
HSSP; P08921; 1HNG.
GO; GO:0005612; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
InterPro; IPR00110; Ig.
InterPro; IPR007110; Ig-like.
Pfam; PF00047; ig; 1.
SMARY; SM00409; IG; 2.
PROSITE; PS50835; IG_LIKE; 2.
 64; Conservative
 Similarity
 NCBI_TaxID=10090;
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"Gene structure of the mouse leukocyte cell surface molecule Ly9."; Immunogenetics 51:788-793(2000).
 PROSITE; PS56835; IG LIKE; 2.
Antigen; Cell adhesion; Direct protein sequencing; Glycoprotein;
Immunoglobulin domain; Polymorphism; Repeat; Signal; Transmembrane.
 (Potential).
(Potential).
(Potential).
(Potential).
(Potential).
(Potential).
 (Potential)
(Potential)
 T-lymphocyte surface antigen Ly-9 Extracellular (Potential).
 Potential.
Cytoplasmic (Potential).
Ig-like V-type 1.
Ig-like C2-type 2.
Ig-like C2-type 2.
Ig-like C2-type 2.
Potential.
 N-linked (GICNAC...) (N-linked (GICNAC...)
 (in Ly9-1)
(in Ly9-1)
(in Ly9-1)
(in Ly9-1)
(in Ly9-1)
(in Ly9-1)
 Potential
 EMBL; AF244131; AAC14997.1; --
EMBL; AF244130; AAC14997.1; --
EMBL; AF245101; AAC13268.2; --
EMBL; AF245101; AAC13268.2; JOINED.
EMBL; AF24556; AAC13268.2; JOINED.
EMBL; AF24556; AAC13268.2; JOINED.
EMBL; AF245509; AAC13268.2; JOINED.
EMBL; AF245509; AAC13268.2; JOINED.
EMBL; AF245509; AAC13268.2; JOINED.
EMBL; AF245510; AAC13268.2; JOINED.
EMBL; AF24659; AAC13268.2; JOINED.
EMBL; AF24659; AAC13268.2; JOINED.
EMBL; AF24650; AAC13268.2; JOINED.
EMBL; AF246591; AAC13268.2; JOINED.
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EMBL; AF346700; AAC13268.2; JOINED.
EMBL; H258P; P08921; IHNG.
 9 4 4 9 4 9
 MGD; MGI:96885; Ly9.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
Pfan; PR00047; ig; 2.
SMART; SM00409; IG; 2.
 CHAIN
DOMAIN
TRANSMEM
DOMAIN
 DISULFID
DISULFID
DISULFID
 DISULFID
CARBOHYD
CARBOHYD
 CARBOHYD
 VARIANT
VARIANT
VARIANT
 CARBOHYD
 CARBOHYD
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 DOMAIN
DOMAIN
DOMAIN
 VARIANT
 SIGNAL
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34 EIEHII-WNC---PPKALALVFYKKDITILDKGYNGRLKVSEDGYSLYMSNLTKSDSGSY 129
 62 SDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENG-SLLLSDLQLADEGTY 120
 121 EVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLEL-SEAFTLNCSHENGTKPS-- 177
 61
 73
 14 GPLSENPRMSQQQIFSPILMIPLLFLIMGLGASGKETPPTVISGMLGGSVTFSLNISKDA
 6 GALS---RASRALRLAPFVYL-LILIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSSTS
 YTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKI 233
 |:| :: | :: | |:| || || || || || yswtre-----dthintydgshtrangsycopdlepytckampusqussqpvri 238
 Gaps
 19;
 / Match 15.2%; Score 183.5; DB 1; Length 654; Local Similarity 27.1%; Pred. No. 1.1e-05; les 64; Conservative 45; Mismatches 108; Indels 19
 362 P -> S.
366 K -> N (in Ly9-1).
377 B -> K (in Ly9-1).
550 M -> I (in Ly9-1).
592 G -> E (in Ly9-1).
283 F -> L (in Ref. 2).
499 T -> P (in Ref. 2).
560 V -> L (in Ref. 2).
561 TPTYENFT -> SPYL (in Ref. 2).
554 TPTYENFT -> SPYL (in Ref. 2).
554 TPTYENFT -> SPYL (in Ref. 2).
P -> S.

K -> N (in Ly9-1).

E -> K (in Ly9-1).

G -> E (in Ly9-1).

G -> E (in Ly9-1).

F -> L (in Ref. 2).

T -> P (in Ref. 2).

T -> L (in Ref. 2).

T -> L (in Ref. 2).

T -> L (in Ref. 2).

T -> L (in Ref. 2).

T -> L (in Ref. 2).

T -> L (in Ref. 2).
 362
366
377
592
2893
560
6647
654 AA;
 178
 CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
 189
 VARIANT
VARIANT
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VARIANT
 Query Match
 Best Loc
Matches
 PTT FFT FFT SO SET
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Search completed: July 26, 2005, 16:12:58 Job time : 62.4446 secs

GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd. Copyright

 protein search, using sw model OM protein July 26, 2005, 15:58:02; Search time 22.1316 Seconds Run on:

(without alignments)
1665.085 Million cell updates/sec

US-10-706-691-26 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|               |        | a              |        |    | SUMMARIES |                    |
|---------------|--------|----------------|--------|----|-----------|--------------------|
| Result<br>No. | Score  | Query<br>Match | Length | DB |           |                    |
|               | 218.5  | 11.1           |        | -  | RWHUC2    | T-cell surface qly |
| 7             | 216    | 11.0           | 341    | 0  | JC1512    | y glycop           |
| m             | 207.5  | 10.6           | 278    | 7  | JC1506    | biliary glycoprote |
| 4             | 202.5  | 10.3           | 278    | ~  | A39037    | w                  |
| S             | 194.5  | 9.9            | 483    | 7  | T17346    | hypothetical prote |
| 9             | 189    | 9.6            | 365    | 7  | JC7780    | coxsackie- and ade |
| 7             | 188.5  | 9.6            | 1001   | ~  | A58532    | _                  |
| 80            | 188    | 9.6            | 341    | 0  | JC1511    | biliary glycoprote |
| 0             | 186.5  | 9.5            | 458    | 7  | JC1509    |                    |
| 10            | 185    | 4.6            | 272    | ~  | 148268    |                    |
| 11            | 181.5  | 6.9            | 521    | 7  | S34338    |                    |
| 12            | 180.5  | 9.5            | 347    | ~  | S41638    | 8                  |
| 13            | 180.5  | 9.5            | 629    | N  | A46500    | Ly-9.2 antigen - m |
| 14            | 179.5  | 9.1            | 278    | 0  | JC1507    | ->                 |
| 15            | •      | 9.0            | 475    | ~  | A54879    | pregnancy-specific |
| 16            | 173.5  | 8.8            | 344    | ٦  | RWRTC2    | T-cell surface qly |
| 17            | 173.5  | 8.8            | 853    | Н  | IJBONC    | neural cell adhesi |
| 18            | 172.5  | 8.8            | 828    | Н  | IJRTNC    | neural cell adhesi |
| 19            | 170.5  | 8.7            | 526    | ٦  | A32164    | biliary glycoprote |
| 20            | 17.0.5 | 8.7            | 1227   | ~  | T23004 .  | hypothetical prote |
| 21            | 168    | 8.6            | 761    | Н  | IJHUNG    | neural cell adhesi |
| 22            | 166    | 8.5            | 458    | ~  | S68177    | C-CAM2a protein is |
| 23            | 166    | 8.5            | 458    | ~  | 823969    | cell-adhesion mole |
|               | 166    | 8.5            | 519    | ~  | A44783    | ecto-ATPase precur |
|               | 166    | 8.5            | 1091   |    | IJCHINT   | neural cell adhesi |
| 56            | 165    | 8.4            | 475    | ~  | 176668    | pregnancy-specific |
| 27            | 164.5  | 8.4            | 299    | •  | S56749    | junctional adhesio |
| 28            | 164    | 8.4            | 464    | ~  | C30127    | embrar             |
| 29            | 163.5  | 8.3            | 725    | ~  | JE0100    | neural cell adhesi |

| neural cell adhesi | biliary glycoprote | biliary glycoprote | neural cell adhesi | neural cell adhesi | neural cell adhesi | nonspecific cross- | carcinoembryonic a | pregnancy-specific | pregnancy-specific | pregnancy-specific | pregnancy-specific | pregnancy-specific | pregnancy-specific | T-cell surface gly | pregnancy-specific |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
|                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |
| IJMSNL             | WMMSR1             | JC1508             | JN0635             | T43027             | IJMSNG             | A27681             | A35364             | G43354             | F43354             | A43354             | H43354             | E43354             | A27658             | B28967             | B54312             |
| 1 IJMSNL           | 1 WMMSR1           | 2 JC1508           | 1 JN0635           | 2 T43027           | 1 IJMSNG           | 2 A27681           | 2 A35364           | 2 G43354           | 2 F43354           | 2 A43354           | 2 H43354           | 2 E43354           | 2 A27658           | 2 B28967           | 2 B54312           |
| Н                  | Н                  | ~                  | 1092 1 JN0635      | ~                  | -                  | ~                  | ~                  | N                  | N                  | ~                  | ~                  | ~                  | 7                  | 7                  | 2<br>E             |
| Н                  | Н                  | ~                  | -                  | ~                  | -                  | 344 2              | 709 2              | 324 2 (            | N                  | 333 2              | ~                  | ~                  | 7                  | 7                  | 2<br>E             |
| Н                  | 8.2 458 1          | 8.2 521 2          | -                  | 8.2 1232 2         | 8.1 725 1          | 8.1 344 2          | 8.1 709 2          | 8.0 324 2 (        | 8.0 326 2          | 8.0 333 2          | 8.0 335 2 1        | 8.0 406 2          | 7                  | 8.0 344 2 1        | 7.9 419 2 B        |

## ALIGNMENTS

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T-cell surface glycoprotein CD2 precursor - human
NyAlternate names: E rosette receptor; erythrocyte receptor; erythrocyte-binding protein
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 09-Jul-2004
C;Accession: A28967; A26466; B26486; A28023; S02292; A30430; S00829; A29874
R;Diamond, D.J.; Clayton, L.K.; Sayre, P.H.; Reinherz, E.L.
R;Diamond, D.J.; Clayton, L.K.; Sayre, P.H.; Reinherz, E.L.
A;Title: Exon-intron organization and sequence comparison of human and murine Til (CD2) of A;Reference number: A28967; MUID:88144486; PMID:2894031

A, Molecule type: DNA

A;Residues: 1-351 <DIA>
A;Cross-references: UNIPROT:P06729; GB:M19806; GB:J03622; GB:J03623; NID:g180079; PIDN:A,
R;Sewell, W.A.; Brown, M.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J.
Proc. Natl. Acad. Sci. U.S.A. 83, 8718-8722, 1986
A;Title: Molecular cloning of the human T-lymphocyte surface CD2 (T11) antigen.
A;Reference number: A26486; MUID:87041523; PMID:3490670

A;Accession: A26486

A;Molecule type: mRNA A;Residues: 1-338,'M',340,'QQKTHCPLPLIKKDRNCLFQ' <SB1> A;Accession: B26486

A,Molecule type: protein (SE2)
A,Residues: 25-46, X',50 (SE2)
R,Sewell, W.A.; Brown, W.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 7256, 1987
A,Reference number: A28416
A,Contents: revision

A;Molecule type: mRNA A;Residues: 333-351 <SE3> P.Seed, B.; Aruffo, A. Proc. Natl. Acad. Sci. U.S.A. 84, 3365-3369, 1987 A;Title: Molecular cloning of the CD2 antigen, the T-cell erythrocyte receptor, by a rap; A;Reference number: A28023; MUID:87204137; PMID:2437578

, Molecule type: mRNA Accession: A28023

A;Readdues: 1-265, 0., 267-351 <SEE>
A;Cross-references: GB:M16445; NID:g178668; PIDN:AAA51738.1; PID:g178669
A;Cross-references: GB:M16445; NID:g178668; PIDN:AAA51738.1; PID:g178669
B;Sayre, P.H.; Chang, H.C.; Hussey, R.E.; Brown, N.R.; Richardson, N.E.; Spagnoli, G.; C]
Proc. Natl. Acad. Sci. US.A. 84, 2941-2945, 1987
A;Title: Molecular cloning and expression of T11 cDNAs reveal a receptor-like structure of A;Reference number: S02292; MUID:87204243; PMID:2883656

A; Accession: S02292

A,Residues: 1-338,'M',340,'QOKTHCPLPLIKKDRNCLFQ' <SA1> A,Cross-references: GB:M16336, NID:g180093; PIDN:AAA51946.1; PID:g180094 A; Molecule type: mRNA

A; Accession: A30430

A;Molecule type: protein A;Residues: 25-43,152-163 <SA2> R;Lang, G.; Wotton, D.; Owen, M.J.; Sewell, W.A.; Brown, M.H.; Mason, D.Y.; Crumpton, M.

us-10-706-691-26.rpr

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Length 341;

Indels

48; Mismatches 125;

11.0%; Score 216; DB 2; 26.1%; Pred. No. 2.9e-06;

126

92

261

```
C;Superfamily: biliary glycoprotein, carcinoembryonic antigen precursor amino-terminal har C;Superfamily: biliary glycoprotein; receptor C;Keywords: glycoprotein; receptor C;Keywords: glycoprotein; raccinoembryonic antigen precursor amino-terminal homology <CEAN>F;139-216/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>F;87,104,153,195/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Cross-references: UNIPROT:099232
Comment: This protein is expressed at the cell surface and plays a determinant role in
 238 QGGLSDGAIAGIVIGVVAGVALIAGLAYFLYSRKSGGGSDQRDLTEHKPSTSNHNLAPSD 297
 F;87,104,153,195/Binding site: carbohydrate (Asn) (covalent) #status predicted
 96 DTF-TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPL 154
 155 LNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSSLYII--- 211
 C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
 : | | | : | | | : | | | : | | | : | | | | : | | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
 40 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITD
 ---LSTG-----GIFLLVTLVTVCACWKPSKRKQKKLEKQNSLEYMDQNDDRLKPEAD
 C,Accession: JC1506
R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N. Gene 127, 173-183, 193,
A;Title: Expression of the Bgp gene and characterization of mouse colon A;Reference number: JC1505; MUID:93273228; PMID:8500759
 298 NSP-----NKVDDVAYTVLNFNSQQPNRPTSAPSSPRATE 332
 262 TLPRSGEQERKNPMALYILKDKDSPETEENPAPEPRSATE 301
 A;Status: nucleic acid sequence not shown
 Query Match
Best Local Similarity 26.19
Matches 73; Conservative
 glycoprotein B - mouse
 A, Residues: 1-278 <MCC>
 A; Molecule type: mRNA
 A; Accession: JC1506
 212
 Query Match
 A;Gene: BgpB
 A; Cross-refe
C; Comment: T
C; Genetics:
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EMBO J. 7, 1675-1682, 1988

A, Title: The structure of the human CD2 gene and its expression in transgenic mice.
A, Reference number: S00829; MUID:89005055; PMID:2901953
A, Molecule type: DNA
A, Residues: 1-351 clans
A, Residues: 1-351 clans
A, Residues: 1-351 clans
A, Residues: 1-351 clans
A, Residues: 1-351 clans
A, Residues: Louis a surface antigen expressed on all peripheral blood T-cells. It appear cor is closely associated with, the erythrocyte receptor.
C, Generics:
A, Gene: GDB: CD2
A, Gorse-references: GDB: 118735; OMIM: 186990
A, Map position: 1p13: 1-1p13: 1
A, Introns: 21/1, 128/1, 205/1, 246/1
C, Superfamily: T-cell surface glycoprotein CD2
C, Reywords: glycoprotein; T-cell; transmembrane protein
F; 1-24/Domain: signal sequence #status predicted clans
F; 25-351/Product: T-cell surface glycoprotein CD2 #status predicted clans
F; 210-224/Domain: signal sequence #status predicted clans
F; 210-234/Domain: intracellular #status predicted clans
F; 89, 141, 150/Binding site: carbohydrate (Asn) (covalent) #status predicted
 11
 245
 242
 RLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLE 126
 127 LSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMV 186
 LEYMDQNDDRLKPEADTLPRSGEQERKNPMALYILKDKDSPETEENPAPEPRSATE--- 301
 84
 GTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPD----YRDRI
 GALGQDINLDIPSFQMSDDIDDIKWEKTSDK------KKIAQFRKEKEKETFKEKDTY
 ENPISQGRSLPVKITVYRRSSLYIILS-TGGIFLLVTLVTVCACWKPSKRKQKKLEKQNS
 GNKVSKESSVEPVSCPEKGLDIÝLIGICGGGSLLMVFVALLVFYITKRKKÓRS-----
 Gaps
 61;
 11.1%; Score 218.5; DB 1; Length 351; 23.6%; Pred. No. 2.1e-06;
 53; Mismatches 148; Indels
 RPPPPGHRVQHQPQKRPPAPSGTQVHQQKGPPLPRPRVQPKPP 338
 -PGPPGYSVS-----PAVPG----RSPGLPIRSARRYPRSP 332
 81; Conservative
 Similarity
 296
 12
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of mouse colon biliary glycoprot

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 96 DTF-TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPL 154
 95
 40 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITD
 6
 | | | | : : | | : | | : | | : | | : | | 185 QLTERMTLSQNNSILRIDPIKREDAGEYQCEISNPVSVKRSNSIKLDI 232
 155 INDSRMILISPDOKVLTITRVIMEDDDLYSCMVENPISQGRSLPVKITV 202
Length 278;
 Indels
DB 2;
10.6%; Score 207.5; DB 2; llarity 32.1%; Pred. No. 7.5e-06; Conservative 32; Mismatches 73;
 Local Similarity
es 54; Conserv
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Diliary glycoprotein H - mouse

Diliary glycoprotein H - mouse

C;Species: Mus musculus (house mouse)

C;Species: Musculus (house mouse)

C;Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 09-Jul-2004

C;Accession: JC1512

R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.

R;McLaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.

A;Title: Expression of the Bgp gene and characterization of mouse colon biliary glycoprody. Reference number: JC1505; MUID:93273228; PMID:8500759

A;Reference number: JC1505; MUID:93273228; PMID:8500759

A;Mclecule type: mRNA

A;Residues: 1-341 <MCC>
A;Cross-references: UNIPROT:Q61354; GB:X67283

C;Comment: This protein is expressed at the cell surface and plays a determinant role in

Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin

C;Keywords: glycoprotein; receptor F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN> F;159-216/Domain: immunoglobulin homology <IMM>

carcinoembryonic antigen mmCGM2 precursor - mouse N;Alternate names: biliary glycoprotein homolog; calcium-dependent cell adhesion moleculo C;Species: Mus musculus (house mouse)

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site on bovine cells
 213
 327
 108
 137
 246
 278
 210 SHFPEPDITHSVACROPKLCAGSAYHKEPWKAMEKAEGTPGPHKMEHGGRVVCSDCNTEVD 329
 161
 138 LVKPSGIRCYVDGSE--EIGNDFKLKCEPKEGSLPLRYEWQK----LSDSQKLPTSWLP 190
 214
 MALYILKOKDSPETEENPAPEPRSATEP---GPPGYSVSPAVPGRSPG-----LPIR 323
 54
 79
 A58532
glial cell membrane glycoprotein LIG-1 precursor - mouse
C.Species: Mus musculus (house mouse)
C.Species: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
 C;Species: Bos primigenius taurus (cattle)
C;Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 09-Jul-2004
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDR-PV-VKWQLKRDKPVTVVQSI----GTEV
 55 IGTLRPDYRDRIRLFEN-----GSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTV
 191 EMTSP---VISVKNASAEYSGTÝTCTVRNRVGSDQCL-LRLDVVPPSNRAGTIAGAVIGŤ
 243 QNSLEYMDQNDDRLKPEADTLPRSGEQERKNPMALYILKDKDSPETE---ENPAPEPRSA
 DVPISRPQVLVASTTVLELSEAFTLNCSHENGTKP-SYTWLKDGKPLLNDSRML----
 --LSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSS-----LYIILST
 215 GGIFLLVTLVTVCACWKPSKRKQKKLEKQNSLEYMDQNDDRLKPEADTLPRSGEQERKNP
 Gaps
 A;Cross-references: UNIPROT:Q8WMV3; GB:AY033651
C;Comment: This protein serves as the primary adenoviral attachment
 63; Mismatches 137; Indels 102;
 Length 365;
 C;Accession: A58532 - - R;Suzuki, Y.; Sato, N.; Tohyama, M.; Wanaka, A.; Takagi, T.
 300 TE-PGPPGYSVSPAVPGRSPGL----PIRSARR----
 Pred. No. 0.00015;
 Score 189; DB 2;
 DLERAPOSP-----TLPPAKVAAPNLSR 347
 SARRYPRSPARSPATGRIHSSPPRAPSSPGRSR
 328 -YPRSPARSPATGRIHSSPPRAPSSP 352
 CYSRGOAFHPOPVSRDSAQPSAPNGP 355
 coxsackie- and adenovirus receptor - bovine
 23.2%;
 91; Conservative
 Similarity
 A, Residues: 1-365 <THO>
 A, Molecule type: mRNA
 A; Accession: JC7780
 A;Contents: Liver
 165
 109
 162
 279
 324
 Query Match
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C; Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 09-Jul-2004
C; Accession: A39037; S13760
R; Purbide, C.; Rojas, M.; Stanners, C.P.; Beauchemin, N.
J. Biol. Chem. 266, 309-315, 1991
A; Title: A mouse carcinoembryonic antigen gene family member is a calcium-dependent cell
A; Reference number: A39037; MUID:91093141; PMID:1985902
A; Accession: A39037
A; Accession: A39037
A; Reference number: A39037; MUID:91093141; PMID:1985902
A; Residues: 1-278 «TUR»
A; Residues: 1-278 «TUR»
A; Residues: 1-278 «TUR»
A; Residues: 1-278 arturs
C; Superfamily: Diliary glycoprotein; transmembrane protein
C; Keywords: cell adhesion; glycoprotein; transmembrane protein
C; Keywords: cell adhesion; glycoprotein; transmembrane protein
F;1-134/Domain: carcinoembryonic antigen precursor amino-terminal homology «CEAN»
F;1-34/Domain: extracellular #status predicted «SIG»
F;35-278/Product: carcinoembryonic antigen mmcGM2 #status predicted «MAT»
F;25-278/Domain: transmembrane #status predicted <TMM>F;289-278/Domain: intracellular #status predicted <INTN>F;873-278/Domain: intracellular #status predicted <INTN>F;87,104,153,195/Binding site: carbohydrate (Asn) (covalent) #status predicted
 υ.
..
 DTF-TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPL 154
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 LOLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHE 138
 NGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPV 198
 GNPPPRITWFKGDRPLSLTERHHLTPDNQLLVVQNVVAEDAGRYTCEMSNTLGTERA--- 164
 199 KITVYRRSSLYIILSTG-----GIF-----LLVTLVTVCACWKPSKRKQKKLEK 242
 95
 Species: Homo sapiens (man)
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 Сарв
 40 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITD
 22 VQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLF---ENGSLLLSD
 Gaps
 hypothetical protein DKFZpS8601624.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: T17346
R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, Bubmitted to the Protein Sequence Database, September 1999
A;Reference number: Z18727
A;Reference number: T17346
A;Reference number: L17346
A;Reference number:
 93;
 6
 DB 2; Length 278;
 155 LNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITV 202
 Length 483;
 74; Indels
 Indels
 A; Experimental source: adult uterus; clone DKFZp58601624 C; Genetics:
 DB 2;
 55; Mismatches 155;
 ch
1 Similarity 32.1%; Pred. No. 1.5e-05;
54; Conservative 31; Mismatches 74
 9.9%; Score 194.5; DB 2
21.5%; Pred. No. 9.4e-05;
 83; Conservative
 Similarity
 A; Note: DKFZp58601624.1
 Query Match
Best Local S
Matches 83
 69
 96
 79
 Best Local
Matches 5
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 C;Genetics:
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J. Biol. Chem. 271, 22522-22527, 1996

A; Title: cDNA cloning of a novel membrane glycoprotein that is expressed specifically in A; Reference number: A58322, MUID:96394313; PMID:8798419
A; Reference number: A58322, MUID:96394313; PMID:8798419
A; Accession: A58532
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: mRNA
A; Residues: 1.1091 & SUZ>
A; Cross-references: UNIPROT:P70193; GB:D78572; NID:91545806; PIDN:BAA11416.1; PID:915458
F; 36-61/Domain: proteoglycan anino-terminal homology < LRR1>
F; 36-61/Domain: proteoglycan anino-terminal homology < LRR2>
F; 36-61/Domain: proteoglycan anino-terminal homology < LRR2>
F; 36-61/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR5>
F; 11-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR5>
F; 12-13/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR6>
F; 14-21/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR8>
F; 14-23/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR9>
F; 22-235/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR9>
F; 22-235/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR9>
F; 28-35/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR9>
F; 38-33/Domain: leucine-rich alpha-2-glycoprotein repeat homology < LRR9>
F; 38-34/Domain: leucine-rich alpha-2-glycoprotein r
 DCISII

Diliary glycoprotein G - mouse

Diliary glycoprotein G - mouse

Diliary glycoprotein G - mouse

Cispecies: Mus musculus (house mouse)

Cispecies: Mus musculus (house mouse)

Cipate: 24-Reb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004

Cipate: 24-Reb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004

Cipate: 24-Reb-1994 #sequence_revision 0f the large gene and characterization of mouse colon biliary glycoprophy. The ference number: JC1505; MUD:93273228; PMID:8500759

A;Reference number: JC1501

A;Residues: 1-341 <MCC>

A;Residues: 1-341 <MCC>

A;Cross-references: UNIPROT:Q61353; GB:X67282
 GTTAR-----LECAATGHPNPQIAWQ--KDG-------GTDFPAARER-RMHVM 653
 SEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVE 187
 NPISQGRSLPVKITVYRRSSLYIILSTG-----GIF-----LLVTLVTVCACWK 231
 232 PSKRKQK-----YLEKQNSLE----- 252
 820 TRKKSEEYSVTNTDETIVPPDVPSYLSSQGTLSDRQETVVRTEGGHQANGHIESNGVCLR 879
 DDRLKPEADTLPRSGEQER-----KNPMALYILKDKD-------SPETE 289
 880 DPSLPPEVDIHSTICROPKLCVGYTREPWKVTEKADRTAAPHTTAHSGSAVCSDCSTDTA 939
 70 -ENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLV-ASTTVLEL 127
 654 PDDDVFFITDVKIDDMGVY----SCTAQNSAGSVSANATLTV-LETPSLAVPLEDRVVTV 708
 12 GTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLF-- 69
 ch 9.6%; Score 188.5; DB 2; Length 1091; I Similarity 21.1%; Pred. No. 0.0006; 79; Conservative 56; Mismatches 122; Indels 117;
 F;440-485/Domain: proteoglycan carboxyl-terminal homology <PCH>
 ENPAPEPRSATEPG 303
 940 YHPQPVPRDSGQPG 953
 290
 Query Match
Best Local S
Matches 79
 128
 188
 253
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C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin. C;Keywords: glycoprotein; receptor F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN> F;7-124/Domain: immunoglobulin homology <IMM1> F;75-124/Domain: immunoglobulin homology <IMM1> F;159-216/Domain: immunoglobulin homology <IMM2> F;71,89;104,153,195/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Gene 127, 173-183, 1993
A,Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopro A,Reference number: JC1505, MUID:93273228; PMID:8500759
 C;Keywords: glycoprotein; receptor
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;160-219/Domain: immunoglobulin homology <IMM1>
F;254-303/Domain: immunoglobulin homology <IMM2>
F;339-396/Domain: immunoglobulin homology <IMM3>
F;339-396/Domain: immunoglobulin homology <IMM3>
F;87,104,148,199,206,210,226,258,290,294,304,333,375/Binding site: carbohydrate (Asn) (c
 ü
 Cross-references: UNIPROT:061351; GB:X67280; Comment: This protein is expressed at the cell surface and plays a determinant role in
 C.Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
 role
C;Comment: This protein is expressed at the cell surface and plays a determinant C;Genetics:
A;Gene: BgpG
 8
 154 LLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSSLY---- 209
 DTF-TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNC-SHENGTKPSYTWLKDGKP 153
 62 YRDRIRLFENGSLILLSDLQLADEGTYEVEISITDDTF-TGEKTINLTVDVPISRPQVLVA 120
 STIVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 264 AYFLYSRKSGGGSDQRDLTEHKPSTSNHNLAPSDNSP----NKVDDVAYTVLNFNSQQP 318
 181 LYSCMVENPISQGRSLPVKITVYRRSSLYII-----LSTG-----GIFLLVTLVTVC 227
 211 EYOCEISNPVSVRRSNSIKLDI-----IFDPTOGGLSDGAIAGIVIGVVAGVALIAGL 263
 ACWKPSKRKQKKLEKONSLEYMDQNDDRLKPEADTLPRSGEQERKNPMALYILKDKDSPE 287
 95
 biliary glycoprotein E - mouse
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: JC1509
 40 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITD
 R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
 30;
 Indels 17;
 Length 458;
 Length 341;
 Query Match 9.6%; Score 188; DB 2; Length 34 Best Local Similarity 25.2%; Pred. No. 0.00015; Matches 64; Conservative 45; Mismatches 115; Indels
 9.5%; Score 186.5; DB 2; 27.4%; Pred. No. 0.00027; atrive 38; Mismatches 83;
 Query Match

Best Local Similarity 27.4%; Pre
Matches 52; Conservative 38;
 288 TEENPAPEPRSATE 301
 NRPTSAPSSPRATE 332
 A; Accession: JC1509
A; Molecule type: mRNA
A; Residues: 1-458 <MCC>
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determinant role

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A;Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopro.
A;Reference number: JC1505; MUID:93273228; PMID:8500759
 Fil-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
Fil60-219/Domain: immunoglobulin homology <IMM1>
Fis63-219/Domain: immunoglobulin homology <IMM2>
Fis39-396/Domain: immunoglobulin homology <IMM3>
Fis39-396/Domain: immunoglobulin homology <IMM3>
Fis87,104,148,199,206,210,226,258,290,294,304,333,375/Binding site: carbohydrate (Asn) (c.
 antigen; carcinoembryonic antigen precursor amino-termin
 member of the carcinoembryonic antigen
 A;Molecule type: mRNA
A;Residues: 1-347 <TAV>
A;Coss-references: UNIPROT:P37998; EMBL:X69884; NID:g1057; PIDN:CAA49511.1; PID:g1058
C;Superfamily: T-cell surface glycoprotein CD2
C;Keywords: glycoprotein; surface antigen; T-cell; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-347/Product: T-cell surface glycoprotein CD2 #status predicted <MAT>
 69 KGNPVSTNAEIVHFVTGTNKTTTGPAHSGRETVYSNGSLLIQRVTVKDTGVYTIE--MTD 126
 154 LLADSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSSLY---- 209
 DTF-TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNC-SHENGTKPSYTWLKDGKP 153
 68 LFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLEL 127
 D.I.; Davis,
 T-cell surface glycoprotein CD2 precursor - horse
N;Alternate names: T-lymphocyte surface antigen CD2
C;Species: Bquus caballus (domestic horse)
C;Date: 13.Jan-1995 #sequence_revision 13.Jan-1995 #text_change 09.Jul-2004
C;Accession: 841638; 831578
R;Tavernor, A.S.; Kydd, J.H.; Bodian, D.L.; Jones, E.Y.; Stuart, D.I.; Davis
Bur. J. Biochem. 219, 969-976, 1994
A;Title: Expression cloning of an equine T-lymphocyte glycoprotein CD2 cDNA.
A;Reference number: 841638; MUID:94155904; PMID:7906650
 40 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITD
 cell surface and plays a
 Indels
 R;Williams, R.K.; Jiang, G.S.; Holmes, K.V.
Proc. Natl. Acad. Sci. U.S.A. 88, 5533-5536, 1991
A;Title: Receptor for mouse hepatitis virus is a member A;Reference number: A410033; MUID:91288498; PMID:1648219
 9.2%; Score 180.5; DB 2;
26.8%; Pred. No. 0.00046;
tive 42; Mismatches 121;
 Query Match 9.3%; Score 181.5; DB 2; Best Local Similarity 27.4%; Pred. No. 0.00065; Matches 52; Conservative 37; Mismatches 84;
 A;Molecule type: mRNA
A;Residues: 1-81,'Q',83-141,'P',143-521 <MCC>
A;Cross-references: GB:X67281
 expressed at the
 Gene: BgpF
Superfamily: carcinoembryonic
Keywords: glycoprotein; recept
 Conservative
 210 IILSTGGIFL 219
 |:| |:|
PIISPSDIYL 251
 A, Molecule type: protein
A, Residues: 35-59 <WIL>
C, Comment: This protein is
 Local Similarity
nes 80; Conserv
 Status: preliminary
 Accession: A41093
 A;Accession: S41638
 187
 Query Match
 Genetics:
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biliary glycoprotein - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 148268
N;Nedellec, P.; Droksler, G.S.; Daniels, E.; Turbide, C.; Chow, B.; Basile, A.A.; Holmes
J. Virol. 68, 4525-4537, 1994
A;Title: Bgp2, a new member of the carcinoembryonic antigen-related gene family, encodes
A;Recession: 148268
A;Accession: 14826
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-272 <RES>
A;Coss-references: UNIPROT:QSRINS; EMBL:X76085; NID:g511020; PIDN:CAA53699.1; PID:g5110
C;Genetics:
A;Gene: Bgp2
C;Superfamily: biliary glycoprotein; carcinoembryonic antigen precursor amino-terminal h
C;Keywords: glycoprotein
C;Keywords: glycoprotein to antigen precursor amino-terminal homology <CEAN>
F;159-216/Domain: immunoglobulin homology <IMM>
 Milary glycoprotein F - mouse
Milary glycoprotein F - mouse
Milary glycoprotein F - mouse
Milary glycoprotein
Milary glycoprotein
C;Species: Mus musculus (house mouse)
C;Becies: Mus musculus (house mouse)
C;Bate: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 09-Jul-2004
C;Bate: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 09-Jul-2004
C;Bate: 20-Feb-1995 #sequence revision Novel, G.
Sibate: 20-Feb-1995 #sequence novel, M.; Novel, G.
Submitted to the EMBL Data Library, July 1992
A;Becretc to the EMBL Data Library, July 1992
A;Reference number: S34338
A;Accession: S34338
 A;Cross-references: UNIPROT:Q61352; EMBL:X67281; NID:g312585; PIDN:CAA47698.1; PID:g3125
R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
57 TLRPDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTF-----TGEKTINLTVDVP 111
 --GPVHSGRETLYSNGSLLIQRVTMKDTGVYTIE--MTDQNYRRRVLTGQ----FHVHKP 143
 ISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTI 171
 172 TRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSSLYI-----ILSTG---GIFLLVT 222
 10 IHGTVGKSALLSV------QYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIG
 9.4%; Score 185; DB 2; Length 272;
.larity 25.7%; Pred. No. 0.00018;
Conservative 45; Mismatches 86; Indels
 210 IILSTGGIFL 219
 |:| |:|
PIISPSDIYL 251
 Similarity
62; Conserv
 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-521 <HUA>
 L 223
 L 262
 43
 Best Local (
Matches 6
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S.J.; Butci

Structure-b.

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Indels

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A,Gene: BgpC

S,Superfamily: biliary glycoprotein; carcinoembryonic antigen precursor amino-terminal hc

C;Superfamily: biliary glycoprotein; receptor

C;Keywords: glycoprotein; receptor

F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>

F;75-124/Domain: immunoglobulin homology <IMMI>

F;15-216/Domain: immunoglobulin homology <IMMI>

F;15-216/Domain: immunoglobulin homology <IMMI>

F;15-216/Domain: immunoglobulin homology <IMMI>

F;15-126/Domain: immunoglobulin homology <IMMI>
 95 YSGREIIYSNGSLLFQMITMKDMGVYTLD--MTDENYRRTQATVRFHVHQPVTQPFLQVT 152
 62 YRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTF-TGEKTINLTVDVPISRPQVLVA 120
 121 STIVLELSEAFILNCSHENGTKPSYIWLKDGKPLLNDSRMLLSPDOKVLTITRVLMEDDD
 9.1%; Score 179.5; DB 2;
llarity 31.7%; Pred. No. 0.0004;
Conservative 29; Mismatches 63;
 Search completed: July 26, 2005, 16:14:17
Job time : 23.1316 secs
 Local Similarity
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 RESULT 13
A46500
Ly-9.2 antigen - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A46500
R;Sandrin, M.S.; Gumley, T.P.; Henning, M.M.; Vaughan, H.A.; Gonez, L.J.; Trapani, J.A.;
J. Immunol. 149, 1636-1641, 1992
A;Title: Isolation and characterization of cDNA clones for mouse Ly-9.
A;Reference number: A46500 MUID:92373005; PMID:1506686
A;Accession: A46500
A;Retus: prellminary
A;Molecule type: mRNA; protein
A;Residues: 1-629 <SAN>
A;Coss-references: GB:M84412; NID:g198931; PIDN:AAA39468.1; PID:g198932
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A;Experimental source: C57BL/6
A;Note: sequence extracted from NCBI backbone (NCBIN:111651, NCBIP:111654)
C;Keywords: transmembrane protein
 Diliary glycoprotein C - mouse billiary glycoprotein C - mouse c.5pecies: mas musculus (house mouse)
C.5pecies: Mas musculus (house mouse)
C.5pecies: Mas musculus (house mouse)
C.5pecies: Mas musculus (house mouse)
C.6Accession: JC1507
R.6McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
R.6McLaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
R.71tle: Expression of the Bgp gene and characterization of mouse colon biliary glycoprod A; Reference number: JC1505; MUID:93273228; PMID:8500759
A;Accession: JC1507
A;Residues: J-278 <MCC>
A;Residues: 1-278 <MCC>
A;Residues: Lais worker (B: K67278
A;Cross-references: UNIPROT:Q61350; GB:K67278
C;Comment: This protein is expressed at the cell surface and plays a determinant role in
 7;
 85 RLKVSEDGYSLYMSNLTKSDSGSYHAQINQKNVILTTNKEFTLHIYEKLQKPQIIVESVT 144
 ----TLTCEVTKGTDFE---LK----LYLNGRMIQKSPRKVIVYKRASNQIAS-FKCTAN 185
 245
 186 NTVSEESSSVVIRCTEKGLDIYLISGICGGGIILFVFLALL--IFVISKRK-----KQNS 238
 RIRLFENG-SLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVASTT 123
 124 VLEL-SEAFTLNCSHENGTKPS--YTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 145 PSDTDSCTFTLICT-VKGTKDSVQYSWTRE-----DTHLNTYDGSHTLRVSQSVCDPDL 197
 246 LEYMDQNDDRLKPEADTLPRSGEQERKNPMALYILKDKDSPETEENPA---PEPRSATEP 302
 ----RRNDEELEIRAHKV--ISEERGRKPHQI-----PGSTPLNPAASQPPPPPSHRP 285
 SEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVE 187
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 55; Conservative
 Similarity
 65
 239
 Query Match
 Best Local
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A;Cross-references: UNIPROT:062664; GB:U09815; NID:9497254; PIDN:AAA56870.1; PID:9497255 A;Note: authors translated the codon GCT for residue 64 as Gly C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termins C;Keywordss: glycoprotein
F;L-137/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA1> F;242-378/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA2> F;399-456/Domain: immunoglobulin homology <IMM2>
 CjAccession: A54879
R;Chen, H.; Chen, C.L.; Chou, J.Y.
Biochemistry 33, 9615-9626, 1994
A;Title: Characterization of two promoters of a rat pregnancy-specific glycoprotein gene A;Reference number: A54879; MUID:94347731; PMID:8068638
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 284 HAVEGESVLLYVH--NLPEALQTFSWYKGVYSLKEFK--IAEYSIATKSVFP-GPAHRGR 338
 66 IRLFENGSLILSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTV- 124
 339 ATGYTNGSLILLODLTARDTGLYTL-VTLDSNSKIKSAPVQVTVHKPVTQPFLRVTESTVT 397
 398 VQSSVVFT--CLSDN-TGVSIRWLFKNQNLQVTERMTLSPSNCQLRIHDVRREDAGQYRC 454
 125 LELSEAFTINCSHENGTKPSYTWIKDGKPLINDSRMILSPDQKVLTITRVIMEDDDLYSC 184
 pregnancy-specific glycoprotein rnCGM3 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
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A;Residues: 1-475 <CHE>
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GenCore version 5.1.6
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OM protein - protein search, using sw model

July 26, 2005, 15:58:52 ; Search time 28.2793 Seconds Run on:

(without alignments) 1011.008 Million cell updates/sec

US-10-706-691-26 Title: Perfect score:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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6: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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|           | Ę              | 320,               | 320,               | 320,               | 320,              | 320,     | 320,               | 320,         | 320,           | 320,              | 6, A            | 6, A            | 2, A            | 2, A            | 13,               |                   | 22,               |                  | 6, A             | 6, A            | 5, A            | 3, A     | 2, A             | 2, A            | 6064,              | 11050,              | . '92             | 24,               |
|           | Description    | Sequence           | Sequence           | Sequence           | Sequence          | Sequence | Sequence           | Sequence     | Sequence       | Sequence          | Sequence        | Sequence        | Sequence        | Sequence        | Sequence          | Sequence          | Sequence          | Sequence         | Sequence         | Sequence        | Sequence        | Sequence | Sequence         | Sequence        | Sequence           | Sequence            | Sequence          | Sequence          |
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|           | DB             | 4                  | 4                  | 4                  | 4                 | 4        | 4                  | 4            | 4              | 4                 | ო               | 4               | m               | ო               | 4                 | н                 | ო                 | 4                | 4                | 4               | m               | 7        | m                | ო               | 4                  | 4                   | e                 | 4                 |
|           | Length         | 450                | 450                | 450                | 450               | 450      | 450                | 450          | 450            | 450               | 351             | 351             | 1101            | 387             | 316               | 319               | 319               | 319              | 319              | 319             | 1091            | 365      | 365              | 365             | 365                | 383                 | 365               | 270               |
| de        | Query<br>Match | 13.7               | 13.7               | 13.7               | 13.7              | 13.7     | 13.7               | 13.7         | 13.7           | 13.7              | 11.1            | 11.1            | 10.2            | 10.0            | 9.9               | 9.7               | 9.7               |                  | 9.7              | o,              |                 |          |                  |                 |                    |                     |                   | 4.6               |
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| , Appl           | , Appl            | , Appl           | Appli           | Appli           | ', Appl           | i, Appl           | Appli           | 24, Appl         | 6428, Ap           | 483, App          | 7327, Ap           | Appli            | 4, Appl           | , Appl           | ', Appl           | , Appl            | , Appl           |  |
|------------------|-------------------|------------------|-----------------|-----------------|-------------------|-------------------|-----------------|------------------|--------------------|-------------------|--------------------|------------------|-------------------|------------------|-------------------|-------------------|------------------|--|
| 24               | 26                | 26               | ď               | 4               | 7                 | 2,                | 9               |                  |                    |                   |                    |                  | Ň                 | Ň                | Ä                 | H                 | ĭ                |  |
| Sequence         | Sequence          | Sequence         | Seguence        | Sequence        | Sequence          | Seguence          | Sequence        | Sequence         | Sequence           | Sequence          | Sequence           | Sequence         | Sequence          | Sequence         | Sequence          | Sequence          | Sequence         |  |
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## ALIGNMENTS

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APPLICANT: Kijavin, Ivar J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Wood, William, I.
APPLICANT: Wood, William, I.
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APPLICANT: Wood, William, I.
APPLICANT: WOOD, WILLIAM, I.
APPLICANT: WOOD APPLICANTON
 FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
APPLICATION NUMBER: PCT/US99/21547
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Sequence 320, Application US/09907794A Patent No. 6635468 GENERAL INFORMATION:
 Godowski, Paul J.
Grimaldi, Christopher J.
 Ferrara, Napoleone
Filvaroff, Ellen
 Kenneth, J
 Gerritsen, Mary E.
Goddard, A.
 Gerber, Hanspeter
 Gurney, Austin L.
 APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
 Fong, Sherman
Gao, Wei-Qiang
 Desnoyers, Lu
Baton, Dan L.
 Hillan,
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PELICANT: WILLIAMS, F. MILCAN, APPLICANT: WILLIAMS, F. MILCAN, APPLICANT: WILLIAMS, F. MILCAN, I TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Enceding the Same CURRENT ON TO 100-107-12 (MIRCANTION: Acids Enceding the Same CURRENT APPLICATION NUMBER: US/09/905,125A (CURRENT APPLICATION NUMBER: US/09/905,125A (CURRENT PILLING DATE: 2000-07-12 (MIRCANTION NUMBER: US/01/41,48 (MIRCANTION NUMBER: US/01/41,48 (MIRCANTION NUMBER: US/01/41,48 (MIRCANTION NUMBER: US/01/41,48 (MIRCANTION NUMBER: US/01/41,49 (MIRCANTION NUMBER: ECT/US99/2054 (MIRCANTION NUMBER: ECT/US99/2054 (MIRCANTION NUMBER: PCT/US99/2054 (MIRCANTION NUMBER: PCT/US99/2056 (MIRCANTION NUMBER: PCT/US99/2056 (MIRCANTION NUMBER: PCT/US99/2056 (MIRCANTION NUMBER: PCT/US99/2056 (MIRCANTION NUMBER: PCT/US99/2056 (MIRCANTION NUMBER: PCT/US99/2056 (MIRCANTION NUMBER: PCT/US99/2059 (MIRCANTION NUMBER: PCT/
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 Williams, P. Mickey Wood, William, I.
 TYPE: PRT
ORGANISM: Homo Sapien
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Mather, Jennie P.
 Sequence 320, Application US/09905125A
Patent No. 6664376
 Perrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritgen, Mary E.
 Pan, James
Paoni, Nicholas F.
 Roy, Margaret Ann
 APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botsein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
 Goddard, A.
 ORGANISM: Homo Sapien
 US-09-907-794A-320
 US-09-905-125A-320
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 ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IILE OF INVENTION: Acids Encoding the Same
 TITLE OF INVENTION: ACIDS ENCOLLING LINE SCHOOL
FILE REFERENCE: 10466-14
CURRENT FILING DATE: 2001-07-10
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CURRENT FILING DATE: 2000-02-2
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Hillan, Kenneth, J.
 Williams, P. Mickey Wood, William, I.
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Stewart, Timothy A.
 Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
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Gerritsen, Mary E.
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Mather, Jennie P.
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 Tumas, Daniel
 TYPE: PRT

CRGANISM: Homo Sapien

US-09-902-775A-320
 Goddard,
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 APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
 10;
13.7%; Score 268; DB 4; Length 450; 31.9%; Pred. No. 1.4e-13; Live 43; Mismatches 90; Indels
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PRIOR FILING DATE: 1999-07-26
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 PRIOR FILING DATE: 1999-07-28
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PRIOR FILING DATE: 1999-09-09
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 APPLICATION NUMBER: PCT/US99/21090
 FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
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 Godowski, Paul J.
Grimaldi, Christopher J.
 Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
 Ferrara, Napoleone
Filvaroff, Ellen
 Hillan, Kenneth, J
 Gao, Wei-Qiang
Gerber, Hanspeter
 Gerritsen, Mary E
 1999-09-13
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Mather, Jennie P.
 Gurney, Austin L.
Query Match
Best Local Similarity 31.9%
Matches 67; Conservative
 GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
 Eaton, Dan L.
 Goddard, A.
 Pan, James
```

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 1 VNITSPVRLIHGTVGKSALLSVQYS--STSSDRPVVKWQLKR--DKPVTVVQSIGTEVIG 56
 APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: GNE.1618P2C12
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CURRENT APPLICATION NUMBER: US/09/903,603A
PRIOR APPLICATION NUMBER: PCT/US00/04414
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13.7%; Score 268; DB 4; Length 450;
Best Local Similarity 31.9%; Pred. No. 1.4e-13;
Matches 67; Conservative 43; Mismatches 90; Indels
 174 VLMEDDDLYSCMVENPISQGRSLPVKITVY 203
 PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/3091
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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LENGTH: 450
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PRIOR FILING DATE: 1999-07-07
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 RESULT 6
US-09-904-920A-320
; Sequence 320, Application US/09904920A
 ORGANISM: Homo Sapien
 US-09-903-603A-320
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 57 TLRPDYRDRIRLF-ENGSLLLSDLQLADEGTYEVEISIT-DDTFTGEKTINLTVDVPISR 114
 115 PQVLV-ASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITR 173
 1 VNITSPVRLIHGTVGKSALLSVQYS--STSSDRPVVKWQLKR--DKPVTVVQSIGTEVIG 56
 20 LKVÍVPSHTVHGVRGQALYLPVHYGFHTPASDIQII-WLFERPHTMPKYLLGSVNKSVVP 78
 Query Match 13.7%; Score 268; DB 4; Length 450; Best Local Similarity 31.9%; Pred. No. 1.4e-13; Matches 67; Conservative 43; Mismatches 90; Indels
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 VTKEDIGNYSCLVRNPVSEMESDIIMPIIY 226
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
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PRIOR PLING DATE: 1999-12-02
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PRIOR FILING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
 Sequence 320, Application US/09903603A
Patent No. 6767995
 Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
 Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
 Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
 Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
 Eaton, Dan L.
 Goddard, A.
 , ORGANISM: Homo Sapien
US-09-906-700-320
 RESULT 5
US-09-903-603A-320
 APPLICANT:
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Sequence 320, Application US/09909064
Patent No. 6818449
 Godowski, Paul J.
Grimaldi, Christopher
 Williams, P. Mickey
Wood, William, I.
 Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Query Match 13.7%;
Best Local Similarity 31.9%;
Matches 67; Conservative 4
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 Kenneth, J
 Gerber, Hanspeter
Gerritsen, Mary E
 aoni, Nicholas F
 FILING DATE: 1999-09-15
 Gurney, Austin L
 Kljavin, Ivar J.
Mather, Jennie P
 Botstein, David
 Genentech, Inc.
Ashkenazi, Avi
 Wei-Oiang
 Eaton, Dan L.
 Goddard, A
 Јатев
 .09-909-064-320
 APPLICANT:
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 PRIOR APPLICATION NUMBER: US 60/145,698
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PRIOR PILING DATE: 1999-07-26
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 FILE REFERENCE: 10466-14
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 Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
 Williams, P. Mickey
Wood, William, I.
 Roy, Margaret Ann
etewart, Timothy A
 Ferrara, Napoleone
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Fong, Sherman
 Pan, James
Paoni, Nicholas F.
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 Wei-Qiang
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 Goddard, A.
 TYPE: PRT
ORGANISM: Homo Sapien
US-09-904-920A-320
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 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITLE OF INVENTION: Acids Encoding the Same
 Gaps
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; Score 268; DB 4; Length 450;
; Pred. No. 1.4e-13;
43; Mismatches 90; Indels
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 FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,064
CURRENT FILING DATE: 2001-07-18
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PRIOR APPLICATION NUMBER: US 60/143,048
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PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
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 FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
 APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
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APPLICATION NUMBER: PCT/US99/23089
 APPLICATION NUMBER: PCT/US99/20594
FILING DATE: 1999-09-08
 APPLICATION NUMBER: PCT/US99/20944
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APPLICANT: WOOD, MILITAM, 1.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE OF INVENTION: Acids Encoding the Same FILE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: US/09/905,381A CURRENT FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-22

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 US-09-906-618-320
; Sequence 320, Application US/09906618
; Patent No. 6828146
 PRIOR FILING DATE: 2000-0
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 320
 TYPE: PRT
ORGANISM: Homo Sapien
US-09-905-381A-320
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 57 TLRPDYRDRIRLF-ENGSLLLSDLQLADEGTYEVEISIT-DDTFTGEKTINLTVDVPISR 114
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 174 VLMEDDDLYSCMVENPISQGRSLPVKITVY 203
PRIOR FILING DATE: 1999-10-05
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PRIOR FILING DATE: 1999-11-29
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PRIOR FILING DATE: 1999-11-30
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PRIOR FILING DATE: 1999-12-02
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
 Sequence 320, Application US/09905381A Patent No. 6818746
 Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
 Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Glang
Gerber, Hanspeter
Gerritsen, Mary E.
 Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
 Pan, James
Paoni, Nicholas F.
 Kljavin, Ivar J.
Mather, Jennie P.
 APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eacon, Dan L.
 Best Local Similarity 31.9
Matches 67; Conservative
 Goddard, A.
 , ORGANISM: Homo Sapien
US-09-909-064-320
 GENERAL INFORMATION:
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APPLICANT:
 Query Match
 APPLICANT:
APPLICANT:
 APPLICANT
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Gaps

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Indels

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57 TLRPDYRDRIRLF-ENGSLLLSDLQLADEGTYEVEISIT-DDTFTGEKTINLTVDVPISR 114
 79 DL--EYQHKFTWMPPNASLLINPLQFPDEGNYIVKVNIQGNGTLSASQKIQVTVDDPVTK 136
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 1 VNITSPVRLIHGTVGKSALLSVQYS--STSSDRPVVKWQLKR--DKPVTVVQSIGTEVIG
 Sequence 6, Application US/08466465

Patent No. 6162432

GENERAL INFORMATION:
APPLICANT: Wallner, Barbara P.
APPLICANT: Cooper, Kevin D.
TITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen
TITLE OF INVENTION: Presenting Cell Driven Skin Conditions Using
TITLE OF INVENTION: Inhibitors of the CD2/LFA-3 Interaction
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CAREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/466,465
FILING DATE:
 Pred. No. 1.4e-13;
 174 VLMEDDDLYSCMVENPISQGRSLPVKITVY 203
 197 VTKEDIGNYSCLVRNPVSEMESDIIMPIIY 226
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08755
FILING DATE: 06-0CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/862,022
FILING DATE: 12-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,969
FILING DATE: 07-0CT-1991
ATTORNEY/AGENT INFORMATION:
 NAME: Myers, Louis (PLM)
REGISTRATION NUMBER: 35,965
REFERNCE/DOCKET NUMBER: BGP-111CP
TELECOMMUNICATION:
TELEPHONE: (617)227-7400
Best Local Similarity 31.9%; Pr
Matches 67; Conservative 43;
 IBM PC compatible
 STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 351 amino acids
 TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO:
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 Boston
 COMPUTER:
 TOPOLOGY:
 US-08-466-465-6
 LENGTH:
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 ## APPLICANT: Tunnas, Daniel
APPLICANT: Tunnas, Daniel
APPLICANT: Williams, Daniel
APPLICANT: Wood, Williams, Daniel
APPLICANT: Wood, Williams, Daniel
APPLICANT: Wood, Williams, Daniel
TITLE OF INVENTION: Acids Encoding the Same
FILE REPRENCE: 10466-14
CURRENT FILING DATE: 2001-07-16
PRIOR PILING DATE: 2000-07-16
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PRIOR PILING DATE: 1999-12-06
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 DB 4; Length 450;
 Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
 Gurney, Austin L.
Hillan, Kenneth, J.
 Timothy A.
 Ferrara, Napoleone
Filvaroff, Ellen
 Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
 Paoni, Nicholas F
 Kljavin, Ivar J.
Mather, Jennie P.
 Roy, Margaret Ann
 Ashkenazi, Avi
Botstein, David
Desnoyers, Iuc
Eaton, Dan L.
 Fong, Sherman
 Stewart, Timo
Tumas, Daniel
 Pan, James
 TYPE: PRT
ORGANISM: Homo Sapien
 US-09-906-618-320
 PPLICANT
 PPLICANT
 PPLICANT
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Gaps 61; Length 351; Indels 11.1%; Score 218.5; DB 3; 23.6%; Pred. No. 1.1e-09; iive 53; Mismatches 148; Query Match 11.1 Best Local Similarity 23.6 Matches 81; Conservative

11;

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142 T----TLTCEVMNGTDPELNLYQDGKHLKLSQRVITHKWTTSLSAK-----FKCTA 188
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 APPLICANT: WT, SHUIAN
APPLICANT: SWEET, RAYMOND
APPLICANT: SWEET, RAYMOND
APPLICANT: TRONGH, ALEMSEGED
ATTILE OF INVENTION: A HUMAN LIG-1 HOWOLOG (HLIG-1)
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
CARDESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
 DB 4;
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 11.1%; Score 218.5; DB 4 23.6%; Pred. No. 1.1e-09;
 OPERATING SYSTEM: DOS
SOFTWARE: FASCESO for Windows Version 2.0
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APPLICATION NUMBER: US/08/986,485
FILING DATE: 08-DEC-1997
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/059,448
FILING DATE: 22-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70264
TELECOMMUNICATION INFORMATION:
 Sequence 2, Application US/08986485
 TELEX: 846169
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1101 amino acids TYPE: amino acid sTRANDEDNESS: single
 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
 610-407-0700
610-407-0701
 Conservative
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
 Query Match
Best Local Similarity
Matches 81; Conserv
 Patent No. 6046030
GENERAL INFORMATION:
 USA
 19482
 ΡA
 STATE: PACOUNTRY:
 RESULT 12
US-08-986-485-2
US-09-730-465-6
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 127 LSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMV 186
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 TITLE OF INVENTION: Method of Prophylaxis or Treatment of Antigen Presenting Cell Driven Skin Conditions Using Inhibitors of the CD2/LFA-3 Interaction
 302 -PGPPGYSVS-----PAVPG----RSPGLPIRSARRYPRSP 332
 296 кререснкуонороккерарьстоунооксерпекуоркер 338
 STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/730,465
FILING DATE: 05-Dec-2000
PRIOR APPLICATION NUMBER: PCT/US92/08755
FILING DATE: 06-OCT-1992
APPLICATION NUMBER: US 07/862,022
FILING DATE: 12-APR-1992
APPLICATION NUMBER: US 07/862,022
FILING DATE: 07-OCT-1991
ATTORNEY/AGENT INFORMATION:
 ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
 NAME: Myers, Louis (PLM)
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BGP-111CP
TELECOMMUNICATION INFORMATION:
 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 APPLICANT: Wallner, Barbara P. Cooper, Kevin D.
 TELEPHONE: (617)227-7400
 INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 amino acids
 Sequence 6, Application US/09730465
Patent No. 6764681
GENERAL INFORMATION:
 (617) 227-5941
 CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES:
 : Boston
 US-09-730-465-6
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Patent No. 6699688
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Patent No. 5712369
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 TYPE: PRT
ORGANISM: Homo sapiens
 US-09-397-243D-13
 US-08-597-495B-22
 US-09-397-243D-13
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 17;
 APPLICANT: Jacobs, Kenneth
APPLICANT: Jacobs, Kenneth
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Mi, Sha
APPLICANT: Genetice Institute, Inc.
APPLICANT: Genetice Institute, Inc.
TILE REFERENCE: 6006B.AJ172A
CURRENT APPLICATION: SECRETED PROFEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6006B.AJ172A
CURRENT FILING DATE: 1998-10-20
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21.3%; Pred. No. 1.9e-07;
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 Similarity 21.3984; Conservative
 MOLECULE TYPE: protein US-08-986-485-2
 TYPE: PRT
ORGANISM: Homo sapiens
linear
TOPOLOGY:
 US-09-175-928-2
 234
 Query Match
Best Local &
 22
 26
 Query Match
 Local
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Matches
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17;
 169 LTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCA 228
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AI --GQFKDRITGSNDPGNASITISHMQPADSGIYICDVNNPPD-FLGQNQGILNVSVLV 138
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9.9%; Score 195; DB 4; I
Best Local Similarity 23.4%; Pred. No. 7.4e-08;
Matches 75; Conservative 60; Mismatches 138;
 APPLICANT: Kornecki, Blizabeth
APPLICANT: Kornecki, Malgorzata B.
ITLE OF INVENTION: Human Platelet F11 Receptor
FILE REFERRNCE: 011.00221
CURRENT APPLICATION NUMBER: US/09/397,243D
CURRENT APPLICATION NUMBER: 60/100,638
PRIOR FILING DATE: 1998-09-16
PRIOR FILING DATE: 1998-09-16
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
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GENERAL INFORMATION:

APPLICANT: Old, Lloyd J.; Welt, Sydney; Ritter, Gerd;

APPLICANT: Simpson, Richard J.; Nice, Edouard; Moritz, R. L.;

APPLICANT: Catimel, B.; Ji, Hong; Burgess, Anthony W.;

APPLICANT: Heath, Joan K.; White, Sara J.; Johnstone, Cameron

TITLE OF INVENTION: Colon Cell And Colon Cancer Cell

TITLE OF INVENTION: Associated Nucleic Acid Molecules, Protein And Peptides

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
CITY: New York
COUNTRY: USA
 110 VPISRPQVLVASTTVLELSEAFTLNC-SHENGTKPSYTWLKDGKPLLNDSRMLLSP-DQK 167
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 22 ISVETPQDVLRASQGKSVTLPCTYHTSTSSREGLIQWDKLLLTHTERVVIWPFSNKNYIH 81
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 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage COMPUTER: IBM P8/2 COMPUTER: IBM P8/2 COMPUTER: IBM P8/2 COMPUTER: IBM P8/2 COMPUTER: IBM P8/2 COMPUTER: IBM P8/2 COMPUTER: IBM P8/2 COMPUTER: OF PED-1996 FILING DATE: 0.2-P6-1996 CLASSIFICATION NUMBER: 0.8/511,876 FILING DATE: 0.4-9-1995 FILING DATE: 0.4-9-1995 FILING DATE: 0.4-9-1995 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. 5712369man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 10.946
REPERCOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
FELEPAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
FURGER: amino acids
COOLOGY: linear
US-08-597-4958-22
 281 KDKDSPETEENPAPEPRSATEPGP 304
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Search completed: July 26, 2005, 16:15:55 Job time : 29.2793 secs

Sequence

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 APPLICANT: Davids, Andrew Robert
APPLICANT: Pagan, Richard Joseph
APPLICANT: Pagan, Richard Joseph
APPLICANT: Power, Christopher Benjamin
APPLICANT: Power, Christine
APPLICANT: Chvatchko, Yolande
APPLICANT: Chvatchko, Yolande
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APPLICANT: Chvatchko, Yolande
TITLE OF INVENTION: Cytokine antagonist molecules
FILE REFERENCE: 674582-2001
CURRENT APPLICATION NUMBER: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/GB03/01851
PRIOR FILING DATE: 2003-04-30
PRIOR FILING DATE: 2002-04-30
PRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 43
SOFTWARE: SeqWin99, version 1.02
SEQ ID NO SE SEQ ID NOS: 43
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 Conservative
; ORGANISM: Homo sapiens
US-10-706-691-26
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 Query Match
Best Local Simil
Matches 383;
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 (without alignments)
1519.387 Million cell updates/sec
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 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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9

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Score

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 EKQNSLEYMDQNDDRLKPEADTLPRSGEQERKNPMALYILKDKDSPETEENPAPEPRSAT 300
EKONSLEYMDONDDRLKPEADTLPRSGEOERKNPMALYILKDKDSPETBENPAPEPRSAT 300
 301 EPGPPGYSVSPAVPGRSPGLPIRSARRYPRSPARSPATGRTHSSPPRAPSSPGRSRSASR 360
 274 EKQNSLEYMDQNDDRLKPEADTLPRSGEQERKNPWALYILKDKDSPETEENPAPEPRSAT
 LYSCMVENPISOGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACWKPSKRKOKKL
 Query Match
100.0%; Score 1962; DB 16; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.1e-126;
Matches 383; Conservative 0; Mismatches 0; Indels 0;
 Sequence 41, Application US/10706691
; Sequence 41, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
 APPLICANT: Davids, Andrew Robert
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Christine
; APPLICANT: Christine
; APPLICANT: Christine
; APPLICANT: Christine
; APPLICANT: Christine
; APPLICANT: Cycokine antagonist molecules
; TITLE OF INVENTION: Cycokine antagonist
; TITLE OF INVENTION: Cycokine antagonist
; CURRENT APPLICATION NUMBER: US/10/706,691
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Seqwin99, version 1.02
; TURD: DATE: DATE: DATE: DATE: DATE: DESCRIPTION NUMBER: Christian LENGRIPTION TLRTAGVHIIREQDEAGPVEISA 383
 361 TLRTAGVHIIREQDEAGPVEISA 383
 394 TLRTAGVHIIREQDEAGPVEISA 416
 TYPE: PRT
ORGANISM: Homo sapiens
 RESULT 3
US-10-706-691-41
 US-10-706-691-41
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 LYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACWKPSKRKQKKL 240
 240
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 153
 STIVLELSEAFILNCSHENGIKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 213
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRWLLSPDQKVLTITRVLMEDDD 180
 LYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACWKPSKRKQKKL 240
 EKONSLEYMDONDDRLKPEADTLPRSGEGERKNPMALYILKDKDSPETEENPAPEPRSAT 300
 EKQNSLEYMDQNDDRLKPEADTLPRSGEQERKNPMALYILKDKDSPETEENPAPEPRSAT 300
 EPGPPGYSVSPAVPGRSPGLPIRSARRYPRSPARSPATGRTHSSPPRAPSSPGRSRSASR 360
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 LYSCMVENPISOGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACMKPSKRKOKKL
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 ö
 Length 416;
 Indels
 Sequence 16, Application US/10706691

Sequence 16, Application US/10706691

Publication No. US20040204352A1

GENERAL INFORMATION:

APPLICANT: Fagan, Richard JOSeph

APPLICANT: Phelps, Christine

APPLICANT: Phelps, Christine

APPLICANT: Chartchko, Yolande

APPLICANT: Chartchko, Yolande

APPLICANT: Christine

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APPLICANT: Christine

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APPLICANT: Christine

APPLICANT: Christine

CURRENT CHILING DATE: 2003-11-12

CURRENT FILING DATE: 2003-04-30

PRIOR FILING DATE: 2003-04-30

PRIOR FILING DATE: 2002-04-30

PRIOR FILING DATE: 2002-04-30

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Seqwin99, version 1.02

SEQ ID NO 16

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TUDE: SEQ ID NO 16

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 100.0%; Score 1962; DB 16;
100.0%; Pred. No. 1.1e-126;
tive 0; Mismatches 0;
 TLRTAGVHIIREQDEAGPVEISA 383
 361 TLRTAGVHIIREQDEAGPVEISA 383
 Conservative
 ORGANISM: Homo sapiens
 Similarity
 383;
 US-10-706-691-16
 Query Match
Best Local S
Matches 383
 181
 61
 94
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241
 Query Match
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 61 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 94 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 153
 STIVLELSEAFILNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 154 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRWLLSPDQKVLTITRVLMEDDD 213
 274 KLEKONSLEYMDQNDDRLKSEADTLPRSGEQERKNPMALYILKDKOSSEPDENPATEPRS 333
 334 TTEPGPPGYSVSPPVPGRSPGLPIRSARRYPRSPARSPATGRIHTSPPRAPSSPGRSRSS 393
 181 LYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACWKPSK--RKQK 238
 KLEKQNSLEYMDQNDDRLKPEADTLPRSGEQERKNPMALYILKDKDSPETEENPAPEPRS 298
 299 ATEPGPPGYSVSPAVPGRSPGLPIRSARRYPRSPARSPATGRTHSSPPRAPSSPGRSRSA 358
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 60
 Query Match 94.3%; Score 1850; DB 16; Length 418; Best Local Similarity 94.5%; Pred. No. 5.4e-119; Matches 364; Conservative 9; Mismatches 10; Indels 2;
Sequence 18, Application US/10706691
; Sequence 18, Application US/10706691
; Publication No. US20040204352A1
; GENERAL INFORMATION:
; APPLICANT: Davids, Andrew Robert
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Phelps, Christopher Benjamin
; APPLICANT: Phower, Christine
; APPLICANT: Goodence, Yolande
; APPLICANT: Goodence, Yolande
; APPLICANT: Goodence, Yolande
; APPLICANT: Goodence, Yolande
; APPLICANT: Goodence, Yolande
; PRIOR REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10/706,691
; CURRENT FILING DATE: 2003-11-12
; PRIOR FILING DATE: 2003-04-30
; PRIOR FILING DATE: 2003-04-30
; PRIOR FILING DATE: 2003-04-30
; NUMBER OF SCO ID NOS: 02-04-30
; SOFTWARE: SeqWin99, version 1.02
; TENDROW.
 359 SRTLRTAGVHIIREQDEAGPVEISA 383
 ||:||||||
SRSLRTAGVQRIREQDESGQVEISA 418
 Sequence 4, Application US/10432103
Publication No. US20040043424A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: U. Dyung Aina M.
APPLICANT: ELLIOTT, VIC, Henry
APPLICANT: THANGAVELU, Kavitha
APPLICANT: THANGAVELU, Kavitha
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-18
 US-10-432-103-4
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 APPLICANT:
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 61 DYRDRIRLFENGSLILSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 94 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 153
 121 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 214 LYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACWKPSKRKQKKL 273
 93
 154 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD
 181 LYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACWKPSKRKQKKL
 34 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 Gaps
 ö
 Length 298;
 ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040043424A1 5831801CD1
US-10-432-103-4
 APPLICANT: GANDHI, Ameena R.
APPLICANT: ARVIZU, Chandra
APPLICANT: YAO, Monique G.
TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS
FILE REFERENCE: PF-0841 PCT
CURRENT FILING DATE: 2003-05-16
PRIOR PALLING DATE: 2003-05-16
PRIOR PLILING DATE: 2000-11-16
PRIOR PLILING DATE: 2000-11-16
SOFTWARE: PERL PROGram
SEQ ID NO.
SEQ ID NO.
 0; Indels
 APPLICANT: WAREN, Bridget A.; XU, Yuming;
APPLICANT: WAREN, Bridget A.; XU, Yuming;
APPLICANT: WIE, Henry; BATRA, Sajeev;
APPLICANT: BURFOND, Neil; GANDHI, Ameena R.;
APPLICANT: TANG, Y. Tom; LU, Dyung Aina M.;
APPLICANT: TANG, Y. Tom; LU, Dyung Aina M.;
APPLICANT: DUGGAN, Brendan M.; BAUGHN, Mariah R.;
APPLICANT: DUGGAN, Brendan M.; BAUGHN, Mariah R.;
APPLICANT: NGUYEN, Danniel B.; AZIMZAI, Yalda;
APPLICANT: YAO, Monique G.; Lal, Preeti G.;
APPLICANT: TRAN, Bao; DING, Li;
APPLICANT: TRAN, Bao; DING, Li;
APPLICANT: TRAN, Bao; DING, Li;
APPLICANT: ATHANGAVELU, Kavitha; RAMKUMAR, Jayalaxmi;
APPLICANT: TRAN, Bao; DING, Li;
APPLICANT: TRAN, Bao; DING, Li;
APPLICANT: AD-YONG, Janiace
TITLE OF INVENT AD-YONG, Janiace
TITLE OF INVENT APPLICATION NUMBER: US, 10/415, 188
CURRENT FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: CT/USO1/49670
PRIOR FILING DATE: 2001-10-26
PRIOR FILING DATE: 2001-27
PRIOR FILING DATE: 2001-27
PRIOR FILING DATE: 2001-27
PRIOR FILING DATE: 2001-27
PRIOR FILING DATE: 2001-27
PRIOR FILING DATE: 2001-27
 66.9%; Score 1312; DB 15;
100.0%; Pred. No. 3.6e-82;
tive 0; Mismatches 0;
 Sequence 7, Application US/10415188 Publication No. US20040049010A1 GENERAL INFORMATION:
 GURURAJAN, Rajagopal
GANDHI, Ameena R.
ARVIZU, Chandra
 274 EKONSLEYMDONDDRLKP 291
 Best Local Similarity 100.0
Matches 258; Conservative
Terrence P.
 TYPE: PRT
ORGANISM: Homo sapiens
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 61 LVTLVTVCACWKPSKRKQKKLEKQNSLEYMDQNDDRLKPEADTLPRSGEQERKNPWALYI 120
 160 MLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFL 219
 220 LVTLVTVCACWKPSKRKQKKLEKQNSLEYMDQNDDRLKPEADTLPRSGEQERKNPMALYI 279
 280 LKDKDSPETEENPAPEPRSATEPGPPGYSVSPAVPGRSPGLPIRSARRYPRSPARG 339
 61 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 1 MLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFL 60
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 60
 Gaps
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 ö
 Query Match S9.0%; Score 1157; DB 15; Length 224; Best Local Similarity 100.0%; Pred. No. 1.2e-71; Matches 224; Conservative 0; Mismatches 0; Indels 0
 Length 207;
 340 RTHSSPPRAPSSPGRSRSASRTLRTAGVHIIREQDEAGPVEISA 383
 0; Indels
 ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040049010A1 382654CD1
US-10-415-188-7
 Sequence 22, Application US/10706691
; Bublication No. US20040204352A1
; GENERAL INFORMATION:
APPLICANT: Davids, Andrew Robert
; APPLICANT: Pagan, Richard Joseph
; APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Chvatchko, Yolande
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Chvatchko, Yolande
; APPLICANT: Boschert, Ursula
; TITLE OF INVENTION: Cytokine antagonist molecules
; FILE REFERENCE: 674582-2001
; CURRENT APPLICATION NUMBER: US/10/706,691
; CURRENT APPLICATION NUMBER: PCT/GB03/01851
; PRIOR FILING DATE: 2003-11-12
; PRIOR FILING DATE: 2003-11-12
; PRIOR PPLICATION NUMBER: GB 0209884.6
; PRIOR FILING DATE: 2002-04-30
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO S: 43
LENGTH: 207
 53.3%; Score 1045; DB 16;
100.0%; Pred. No. 5.4e-64;
ive 0; Mismatches 0;
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: US 60/251,825
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/255,085
PRIOR FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 7
LENGTH: 224
 Query Match
Best Local Similarity 100.
Matches 207; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
US-10-706-691-22
 TYPE: PRT
ORGANISM: Homo sapiens
 US-10-706-691-22
 FEATURE
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121 STIVLELSEAFILNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 61 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 94 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 153
 121 STIVLELSEAFILNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 34 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 93
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 Gaps
 ö
 Length 240;
 Indels
 APPLICANT: Payda, Andrew Robert
APPLICANT: Payda, Richard Joseph
APPLICANT: Padan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Power, Christine
APPLICANT: Chvatchko, Yolande
APPLICANT: Chvatchko, Yolande
APPLICANT: Boschert, Ursula
TITLE OF THING DATE: 2003-11-12
CURRENT APPLICATION NUMBER: US/10/706,691
CURRENT FILING DATE: 2003-11-12
PRIOR FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: GB 0209884.6
PRIOR FILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 43
SOFTWARE: SeqWin99, version 1.02
SEQ ID NO 20
LENGTH: 240
 Query Match 53.3%; Score 1045; DB 16; Best Local Similarity 100.0%; Pred. No. 6.5e-64; Matches 207; Conservative 0; Mismatches 0;
 APPLICANT: Davids, Andrew Robert
APPLICANT: Fagan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Power, Christine
APPLICANT: Chvatchko, Yolande
APPLICANT: Boschert, Ursula
TITLE OF INVENTION: Cytokine antagonist molecules
FILE REPERENCE: 674582-2001
 LYSCMVENPISQGRSLPVKITVYRRSS 240
 181 LYSCMVENPISQGRSLPVKITVYRRSS 207
 181 LYSCMVENPISQGRSLPVKITVYRRSS 207
 181 LYSCMVENPISQGRSLPVKITVYRRSS 207
 Sequence 43, Application US/10706691 Publication No. US20040204352A1 GENERAL INFORMATION:
 Sequence 20, Application US/10706691
Publication No. US20040204352A1
GENERAL INFORMATION:
 ORGANISM: Homo sapiens
 US-10-706-691-43
 US-10-706-691-20
 US-10-706-691-20
 61
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STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 154 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 213
 61 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 94 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 153
 34 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 ö
 TITLE OF INVENTION:
TITLE OF INVENTION:
FILE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/112,944

CURRENT APPLICATION NUMBER: US 09/488,725

PRIOR PRILING DATE: 2000-01-28

PRIOR PRILING DATE: 2000-01-25

PRIOR APPLICATION NUMBER: US 09/491,404

PRIOR PILING DATE: 2000-01-25

PRIOR APPLICATION NUMBER: US 09/496,914

PRIOR APPLICATION NUMBER: US 09/496,914

PRIOR PILING DATE: 2000-02-03

PRIOR PILING DATE: 2000-02-03

PRIOR PILING DATE: 2000-03-07

PRIOR PILING DATE: 2000-03-07

PRIOR APPLICATION NUMBER: US 09/519,705

PRIOR APPLICATION NUMBER: US 09/52,929

PRIOR PILING DATE: 2000-03-31

PRIOR PILING DATE: 2000-03-31

PRIOR PILING DATE: 2000-04-18

PRIOR FILING DATE: 2000-05-18

PRIOR FILING DATE: 2000-05-18

PRIOR FILING DATE: 2000-05-18

PRIOR FILING DATE: 2000-05-18

PRIOR PILING DATE: 2000-05-18

PRIOR FILING DATE: 2000-05-18

PRIOR FILING DATE: 2000-05-18

PRIOR PILING DATE: 2000-05-18

PRIOR FILING DATE: 2000-05-18

PRIOR F
 Length 256;
 Indels
 Query Match 52.4%; Score 1029; DB 15;
Best Local Similarity 96.2%; Pred. No. 8.9e-63;
Matches 203; Conservative 5; Mismatches 3;
 181 LYSCMVENPISQGRSLPVKITVYRRSSLYII
 Sequence 880, Application US/10112944
Publication No. US20040048249A1
GENERAL INFORMATION:
SOFTWARE: pt_FL_genes Version 5.0 SEQ ID NO 434 LENGTH: 256
 Wang, Jian-Rui
Wehrman, Tom
Ghosh, Malabika
Wang, Dunrui
Zhao, Qing A.
Wang, Zhiwei
 APPLICANT: Tang, Y. Tom
APPLICANT: Yang, Yonghong
APPLICANT: Weng, Gezhi
 Zhang, Jie
Ren, Feiyan
Xue, Aidong J.
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-112-944-434
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 61 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 94 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 153
 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 34 VNITSPVRLIHGTVCKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 93
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 Gaps
 ô
 APPLICANT: Ghosh, Malabika
APPLICANT: Ghosh, Malabika
APPLICANT: Ghosh, Malabika
APPLICANT: Alao, Qing A.
APPLICANT: Alao, Qing A.
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
TITLE OF INVENTION: No. US20040048249Alel Nucleic Acids and
TITLE OF INVENTION: Secreted Polypeptides
TITLE OF INVENTION: Socreted Polypeptides
TITLE OF INVENTION: No. US2004012.944
CURRENT APPLICATION NUMBER: US 09/488,725
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/519,705
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
 53.3%; Score 1045; DB 16; Length 246; 100.0%; Pred. No. 6.7e-64; cive 0; Mismatches 0; Indels 0
 CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/GB03/01851
PRIOR FILING DATE: 2003-04-30
PRIOR FILING DATE: 2002-04-30
PRIOR FILING DATE: 2002-04-30
SOFTWARE: SeqWin99, version 1.02
LENGTH: 246
 214 LYSCMVENPISQGRSLPVKITVYRRSS 240
 181 LYSCMVENPISQGRSLPVKITVYRRSS 207
 CURRENT APPLICATION NUMBER: US/10/706,691
 APPLICATION NUMBER: US 09/552,929
FILING DATE: 2000-04-18
APPLICATION NUMBER: US 09/577,408
FILING DATE: 2000-05-18
 Sequence 434, Application US/10112944
Publication No. US20040048249A1
GENERAL INFORMATION:
 APPLICANT: Tang, Y. Tom
APPLICANT: Yang, Yonghong
APPLICANT: Weng, Gezhi
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Xue, Aidong J.
 Query Match 53.3
Best Local Similarity 100.
Matches 207; Conservative
 Wehrman, Tom
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-43
 US-10-112-944-434
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Length 114; Indels 9 64

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5 VNIŢSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 61 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDV 110
 65 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDV 114
 TITLE OF INVENTION: Cytokine antagonist molecules
FILE REFERENCE: 674582-2001
CURRENT APPLICATION NUMBER: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/GB03/01851
PRIOR FILING DATE: 2003-04-30
PRIOR FILING DATE: 2003-04-30
PRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 43
SOFTWARE: SeqWin99, version 1.02
SEQ ID NO 4
 Query Match 27.9%; Score 548; DB 16; Best Local Similarity 100.0%; Pred. No. 3.9e-30; Matches 110; Conservative 0; Mismatches 0;
 TYPE: PRT
ORGANISM: Homo sapiens
 ORGANISM: Homo sapiens
 US-10-706-691-14
 US-10-706-691-4
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 94 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLGA 153
 154 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRWLLSPDQKVLTITRVLMEDDD 213
 61 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 34 VNITSPVRLIHGITTUGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 93
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 60
 1 VNITSPVRLIHGITVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 60
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 Gaps
 61 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDV 110
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDV 110
 ;
0
 51.9%; Score 1018; DB 15; Length 256; 96.6%; Pred. No. 5.1e-62; ive 4; Mismatches 3; Indels 0;
 27.9%; Score 548; DB 16; Length 110; 100.0%; Pred. No. 3.8e-30;
 0; Indels
 Sequence 24, Application US/10706691
| Sequence 24, Application US/10706691
| Publication No. US0040204352A1
| GENERAL INFORMATION:
| APPLICANT: Pagan, Richard Joseph
| APPLICANT: Phelps, Christopher Benjamin
| APPLICANT: Phelps, Christopher Benjamin
| APPLICANT: Phelps, Christine
| APPLICANT: Phelps, Christine
| APPLICANT: Chartchko, Yolande
| APPLICANT: Chartchko, Yolande
| APPLICANT: Christine
| APPLICANT: Christine
| PRICANT: Christine
| PRIC
 100.0%; Pred. No. -
 181 LYSCMVENPISQGRSLPVKITVYRRSSL 208
 214 LYSCVVENPINQGRTLPCKITEYRKSSL 241
 Sequence 4, Application US/10706691
Publication No. US20040204352A1
GENERAL INFORMATION:
APPLICANT: Davids, Andrew Robert
APPLICANT: Fagan, Richard Joseph
APPLICANT: Phener, Christopher Benjamin
APPLICANT: Power, Christine
APPLICANT: Chvatchko, Yolande
 Best Local Similarity 100.0
Matches 110; Conservative
 Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
 Best Local Similarity
Matches 201; Conserv
US-10-112-944-880
 RESULT 12
US-10-706-691-24
 US-10-706-691-24
 RESULT 13
US-10-706-691-4
 61
 121
 Query Match
 Query Match
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284 DSPETEENPAPEPRSATEPGPPGYSVSPAVPGRSPGLPIRSARRYPRSPARSPATGRTHS 343
 1 DSPETEENPAPEPRSATEPGPPGYSVSPAVPGRSPGLPIRSARRYPRSFARSPATGRTHS 60
 ö
 Query Match 26.6%; Score 522; DB 16; Length 100; Best Local Similarity 100.0%; Pred. No. 2e-28; Matches 100; Conservative 0; Mismatches 0; Indels
 344 SPPRAPSSPGRSRSASRTLRTAGVHIIREQDEAGPVEISA 383
Sequence 14, Application US/10706691

Sequence 14, Application US/10706691

GENERAL INFORMATION:
APPLICANT: Pagan, Richard Joseph
APPLICANT: Pagan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Christine
APPLICANT: Christine
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APPLICANT: Christine
APPLICANT: Cytokine antagonist molecules
TITLE OF INVENTION: Cytokine antagonist
CURRENT APPLICATION NUMBER: US/10/706,691
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: GB 0209884.6
PRIOR APPLICATION NUMBER: GB 0209884.6
PRIOR APPLICATION NUMBER: GB 0209884.6
NUMBER OF SEQ ID NOS: 43
SOFTWARE: SeqWin99, version 1.02
SEQ ID NO 14.
 RESULT 15
US-10-706-691-6
; Sequence 6, Application US/10706691
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Length 94;
 Query Match 24.7%; Score 484; DB 16; Length 9. Best Local Similarity 100.0%; Pred. No. 7.8e-26; Matches 94; Conservative 0; Mismatches 0; Indels
 GENERAL INFORTATION:
GENERAL INFORTATION:
APPLICANT: Padan, Richard Joseph
APPLICANT: Pable General Joseph
APPLICANT: Phelbs, Christopher Benjamin
APPLICANT: Power, Christine
APPLICANT: Chvatchko, Yolande
APPLICANT: Boschert, Ursula
TITLE OF INVENTION: Cytokine antagonist molecules
FILE REFERENCE: 674582-2001
CURRENT APPLICATION WUMBER: US/10/706,691
CURRENT APPLICATION NUMBER: PCT/GB03/01851
PRIOR APPLICATION NUMBER: PCT/GB03/01851
PRIOR FILING DATE: 2003-04-30
PRIOR FILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 43
SOFTWARE: SeGWIN99, version 1.02
SEQ ID NO 6
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SEQ ID NO 6
SEQ ID NO 6
SEQ ID NO 6
SEQ ID NO 6
SEQ
Publication No. US20040204352A1
 TYPE: PRT;
CRGANISM: Homo sapiens
US-10-706-691-6
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Search completed: July 26, 2005, 16:21:19 Job time: 99.0554 secs

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
 Copyright
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- protein search, using sw model OM protein July 26, 2005, 15:54:21 ; Search time 108.506 Seconds Run on:

(without alignments) 1365.166 Million cell updates/sec

US-10-706-691-26

1962 1 VNITSPVRLIHGTVGKSALL......TAGVHIIREQDEAGPVEISA 383 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_16Dec04:\* Database :

geneseqp1980s: \*
geneseqp2000s: \*
geneseqp2000s: \*
geneseqp2001s: \*
geneseqp2001s: \*
geneseqp2003bs: \*
geneseqp2003bs: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

|    |        | Description | Ado47895 Human mat | Abq75379 Predicted | Abg75377 Human INS | Ado47892 Human pro | Human    | Abg75378 Murine IN | Add65357 Novel hum | Aae14784 Human imm | Ado47890 Human mat | Ado47887 Human pro | Ads11055 Human the | Aae26421 Human tra | Abg75380 INSP052 e | Adm87341 Human pro | Aam24238 Human EST | Adm87787 Human EST | Ads12269 Human the | Ads12268 Human the | Abg75371 Human INS | Abg75376 Human INS | Abg75372 Human INS | Aam78339 Human pro | Aay13398 Amino aci | Adc78632 Human PRO | Aab80266 Human PRO |
|----|--------|-------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
|    |        | e e         | ADO47895           | ABG75379           | ABG75377           | ADO47892           | ADS11056 | ABG75378           | ADQ65357           | AAE14784           | ADO47890           | ADO47887           | ADS11055           | AAE26421           | ABG75380           | ADM87341           | AAM24238           | ADM87787           | ADS12269           | ADS12268           | ABG75371           | ABG75376           | ABG75372           | AAM78339           | AAY13398           | ADC78632           | AAB80266           |
|    |        | DB          |                    | 7                  | 7                  | œ                  | æ        | 7                  | ω                  | 2                  | œ                  | ω                  | œ                  | S                  | 7                  | В                  | 4                  | œ                  | œ                  | 8                  | 7                  | 7                  | 6                  | 4                  | N                  | c                  | 4                  |
|    |        | Length DB   | 383                | 416                | 416                | 416                | 416      | 418                | 367                | 298                | 237                | 270                | 270                | 224                | 246                | 256                | 256                | 256                | 256                | 256                | 114                | 100                | 188                | 338                | 450                | 450                | 450                |
| de | Query  | Match       | 100.0              | 100.0              | 100.0              | 100.0              | 100.0    | .94.3              | 67.2               | 6.99               | 60.8               | 60.8               | 60.8               | 59.0               | 53.3               | 52.4               | 51.9               | 51.9               | 51.9               | 51.9               | 27.9               | 26.6               | 24.7               | 13.7               | 13.7               | 13.7               | 13.7               |
|    |        | Score       | 1962               | 1962               | 1962               | 1962               | 1962     | 1850               | 1318.5             | 1312               | 1192               | 1192               | 1192               | 1157               | 1045               | 1029               | 1018               | 1018               | 1018               | 1018               | 548                | 522                | 484                | 268                | 268                | 268                | 268                |
|    | Result | No.         | -                  | 8                  | m                  | 4                  | Ŋ        | 9                  | 7                  | 80                 | თ                  | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 | 17                 | 18                 | 19                 | 20                 | 21                 | 22                 | 23                 | 24                 | 25                 |

| Aau12360 Human PRO<br>Aau81958 Human PRO<br>Abu71644 Human PRO | Abol17804 Novel hum<br>Abu71499 Human PRO | Human B                  | Abu66758 Human PRO<br>Abu54401 Human sec |                          | Human                    | Human                    | Human                    | Human<br>Novel           |
|----------------------------------------------------------------|-------------------------------------------|--------------------------|------------------------------------------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|
| 4 AAU12360<br>5 AAU81958<br>6 ABU71644                         | 6 ABO17804<br>6 ABU71499<br>6 ABU71499    | 6 ABU71945<br>6 ABO01828 | 6 ABU66758<br>6 ABUS4401                 | 6 ABO47416<br>6 ABU59839 | 6 ABO25029<br>6 ABU64553 | 6 ABU67399<br>6 ABO14919 | 6 ABU67034<br>6 ABU69676 | 6 ABO14858<br>6 ADA45897 |
| 450<br>450<br>450                                              | 450                                       | 450                      | 450 (                                    | 450 (                    | 450 6                    | 450                      | 450 6                    | 450 6                    |
| 13.7<br>13.7<br>13.7                                           | 13.7                                      | 13.7                     | 13.7                                     | 13.7                     | 13.7                     | 13.7                     | 13.7                     | 13.7                     |
| 268<br>268<br>268                                              | 268                                       | 268<br>268<br>268        | 268<br>268                               | 268<br>268               | 268<br>268               | 268                      | 268<br>268               | 268<br>268               |
| 26<br>27<br>28                                                 | 30 5                                      | 333                      | 34<br>35                                 | 36<br>37                 | 38                       | 4 4<br>1 0 1             | 4 4<br>3 2 5             | 4 4<br>5                 |

## ALIGNMENTS

immunosuppressive; antiarteriosclerotic; hypotensive; osteopathic; antianaemic; neuroprotective; nootropic; antiparkinsonian; antiasthmatic; antianaemic; antianaemic; ordiani; HIV; viral infection; cancer; inflammation; allergy; graft rejection; atherosclerosis; hypotension; osteoporosis; anaemia; Alzheimer's disease; Parkinson's disease; asthma; human, virucide, anti-HIV, cytostatic, antiinflammatory, antiallergic; diabetes; myocardial infarction; haemophilia. ADO47895 standard; protein; 383 AA. Human mature protein SEQ ID NO:12. (first entry) 15-JUL-2004 AD047895; RESULT 1 AD047895 

Homo sapiens

WO2004007672-A2.

22-JAN-2004.

09-JUL-2003; 2003WO-US021703.

12-JUL-2002; 2002US-0395402P

(NUVE-) NUVELO INC.

Tang YT; Wehrman T, Wang ZW, Wang J, Zhou P, Rupp F,

WPI; 2004-122914/12. N-PSDB; ADO47893

New isolated polypeptides and polynucleotides useful in diagnostics, forensics, in preventing or treating diseases such as HIV and cancer, and

Claim 10; SEQ ID NO 12; 205pp; English.

as drug targets.

The invention relates to novel isolated polymucleotides and polypeptides encoded by them. Also included are mutants or variants of the polymucleotides and polypeptides. A polypeptide of the invention has virucide, anti-HIV, cytostatic, antiinflammatory, antiallergic, immunosuppressive, antiarteriosclerotic, hypotensive, osteopathic, antianaemic, neuroprotective, nootropic, antiparkinsonian, antiasthmatic, haemostatic, and cardiant activity. The composition and

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methods are useful in diagnostics, forensics, gene or chromosome mapping, identification of mutations responsible for genetic disorders or other traits, in assessing biodiversity, or in producing many other types of data and products dependent on DNA and amino acid sequences. They may also be used in preventing or treating diseases (e.g. HIV and other viral infections, cancer, inflammation, allergies, graft rejection, atheroselerosis, hypertension, osteoporosis, anaemia, Albreimer's disease, Parkinson's disease, asthma, diabetes, myocardial infarction or haemophilia). They may also be used as targets in drug screening. The present sequence represents a polypeptide of the invention.
 240
 LYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACWKPSKKKKKK 240
 300
 EPGPPGYSVSPAVPGRSPGLPIRSARRYPRSPARSPATGRTHSSPPRAPSSPGRSRSASR 360
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 STIVLELSEAFILNCSHENGIKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 STIVLELSEAFILINCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 EPGPPGYSVSPAVPGRSPGLPIRSARRYPRSPARSPATGRTHSSPPRAPSSPGRSRSASR 360
 EKONSLEYMDONDDRLKPEADTLPRSGEOERKNPMALYILKDKDSPETEENPAPEPRSAT 300
 9
 9
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSBRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 EKONSLEYMDONDDRLKPEADTLPRSGEOERKNPMALYILKDKDSPETEENPAPEPRSAT
 LYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACWKPSKRKQKKL
 INSP052; human; cell proliferation; autoimmune disease; inflammation; cardiovascular disease; neurological disease; psychiatric disease; developmental disease; metabolic disorder; infection; immunoglobulin domain-containing cell surface recognition molecule.
 Gaps
 ö
 100.0%; Score 1962; DB 8; Length 383; 100.0%; Pred. No. 2.7e-134;
 0; Indels
 0; Mismatches
 TLRTAGVHIIREQDEAGPVEISA 383
 ABG75379 standard; protein; 416 AA.
 2002GB-00009884.
 30-APR-2003; 2003WO-GB001851
 (first entry)
 Predicted INSP052 protein.
 Matches 383; Conservative
 SA.
 (ARES-) ARES TRADING
 Similarity
 Sequence 383 AA;
 WO2003093316-A2.
 30-APR-2002;
 22-APR-2004
 13-NOV-2003
 121
 181
 241
 301
 61
 ABG75379;
 Query Match
 61
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 The present invention provides the protein and coding sequences of a novel human immunoglobulin domain-containing cell surface recognition molecule known as INSP052. The polypeptide is useful as immunoglobulin domain-containing cell surface recognition molecule. The sequences may also be used in therapy or diagnosing a disease or in the manufacture of a medicament for treating a disease. The disease is a cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, psychiatric, developmental, genetic or metabolic disorder, an infection or other pathological condition. The polypeptides and nucleic acids are essential to the structural integrity and homeostatic functioning of most tissues. The present sequence is a polypeptide shown in the invention
 120
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 153
 STIVLELSEAFTLINCSHENGTKPSYTWLKDGKPLLINDSRMLLSPDQKVLTITRVLMEDDD 180
 213
 273
 EPGPPGYSVSPAVPGRSPGLPIRSARRYPRSPARSPATGRTHSSPPRAPSSPGRSRSASR 393
 93
 New INSP052 polypeptides and nucleic acids, useful in diagnosing and treating cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, psychiatric, developmental, genetic or metabolic disorder.
 STIVLELSEAFTINCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD
 LYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACWKPSKRKQKKL
 EPGPPGYSVSPAVPGRSPGLPTRSARRYPRSPARSPATGRTHSSPPRAPSSPGRSRSASR
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA
 LYSCMVENPI SOGRSLPVKI TVYRRSSLYI I LSTGGI FLLVTLVTVCACWKPSKRKQKKL
 EKQNSLEYMDQNDDRLKPEADTLPRSGEQERKNPMALYILKDKDSPETEENPAPEPRSAT
 INSP052; human; cell proliferation; autoimmune disease; inflammation; cardiovascular disease; neurological disease; psychiatric disease; developmental disease; metabolic disorder; infection; immunoglobulin domain-containing cell surface recognition molecule.
 ö
 Length 416;
 Indels
 100.0%; Score 1962; DB 7;
100.0%; Pred. No. 3e-134;
tive 0; Mismatches 0;
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 Power
 416
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Phelps CB,
 TLRTAGVHIIREQDEAGPVEISA
 ABG75377 standard; protein; 416
 Human INSP052 complete protein.
 Example 2; Fig 5; Opp; English
 (first entry)
 Conservative
 Fagan RJ,
 WPI; 2003-903655/82.
 Query Match
Best Local Similarity
Matches 383; Conserv
 N-PSDB; ACH01277
 Sequence 416 AA;
 22-APR-2004
 Davids AR,
 61
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 154
 181
 214
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 334
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 ABG75377;
 RESULT 3
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Human protein SEQ ID NO:9.

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15-JUL-2004

ADO47892;

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 120
 300
 240
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 153
 213
 333
 novel human immunoglobulin domain-containing cell surface recognition molecule known as INSP052. The polypeptide is useful as immunoglobulin domain-containing cell surface recognition molecule. The sequences may also be used in therapy or diagnossing a disease or in the manufacture of a medicament for treating a disease. The disease is a cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, psychiatric, developmental, ganetic or metabolic disorder, an infection or other pathological condition. The polypeptides and nucleic acids are essential to the structural integrity and homeoscatic functioning of most tissues. The present sequence is a polypeptide shown in the invention
 93
 New INSP052 polypeptides and nucleic acids, useful in diagnosing and treating cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, psychiatric, developmental, genetic or metabolic disorder.
 EKONSLEYMDONDDRIKPEADTLPRSGEOERKNPMALYILKDKDSPETEENPAPEPRSAT
 EPGPPGYSVSPAVPGRSPGLPIRSARRYPRSPARSPATGRTHSSPPRAPSSPGRSRSASR
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA
 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLT1TRVLMEDDD
 STIVLELSEAPTLNCSHENGTKPSYIWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD
 LYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACWKPSKRKQKKL
 LYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACWKPSKRKQKKL
 EKONSLEYMDONDDRLKPEADTLPRSGEOERKNPMALYILKDKOSPETEENPAPEPRSAT
 EPGPPGYSVSPAVPGRSPGLPIRSARRYPRSPARSPATGRTHSSPPRAPSSPGRSRSASR
 present invention provides the protein and coding sequences of
 ;
0
 DB 7; Length 416;
 Indels
 Query Match 100.0%; Score 1962; DB 7; Best Local Similarity 100.0%; Pred. No. 3e-134; Matches 383; Conservative 0; Mismatches 0;
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 Power
 TLRTAGVHIIREQDEAGPVEISA 383
 Phelps CB,
 Claim 1; Page 67; Opp; English
 30-APR-2003; 2003WO-GB001851
 30-APR-2002; 2002GB-00009884
 Davids AR, Fagan RJ,
 TRADING
 WPI; 2003-903655/82.
 N-PSDB; ACH01275
 Sequence 416 AA;
 WO2003093316-A2.
 Homo sapiens
 (ARES-) ARES
 13-NOV-2003
 61
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The invention relates to novel isolated polymucleotides and polypeptides encoded by them. Also included are mutants or variants of the encoded by them. Also included are mutants or variants of the polymetides. A polymeptide of the invention has virucide, anti-HIV, cytostatic, antiinflammatory, antiallergic, immunosuppressive, antiarteriosclerotic, hypotensive, osteopathic, antianaemic, neuroprotective, nootropic, antiparkinsonian, antiasthmatic, haemostatic, antidiabetic, and cardiant activity. The composition and methods are useful in diagnostics, forensics, gene or chromosome mapping, identification of mutations responsible for genetic disorders or other traits, in assessing biodiversity, or in producing many other types of data and products dependent on DNA and amino acid sequences. They may also be used in preventing or treating diseases (e.g. HIV and other viral infections, cancer, inflammation, allergies, graft rejection, atherosclerosis hypertension, osteoporosis, ansemia, Alzheimer's disease, Parkinson's disease, asthma, diabetes, myocardial infarction or haemophilia). They may also be used as targets in drug screening. The present sequence represents a polypeptide of the invention.
 immunosuppressive, antiarteriosclerotic; hypotensive; osteopathic; antianaemic; neuroprotective; nootropic; antiparkinsonian; antiasthmatic; haemostatic; antidiabetic; cardiant; HIV; viral infection; cancer; inflammation; allergy; graft rejection; atherosclerosis; hypertension; osteoporosis; anaemia; Alaheimer's disease; Parkinson's disease; asthma; diabetes; myocardial infarction; haemophilia.
 New isolated polypeptides and polynuclectides useful in diagnostics, forensics, in preventing or treating diseases such as HIV and cancer, and as drug targets.
 120
 153
 180
 213
 9
 93
 human; virucide; anti-HIV; cytostatic; antiinflammatory; antiallergic;
 34 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA
 STIVLELSEAFILNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 ö
 100.0%; Score 1962; DB 8; Length 416; 100.0%; Pred. No. 3e-134; ive 0; Mismatches 0; Indels 0
 Tang YT;
 Wang ZW,
 Wehrman T,
 Claim 10; SEQ ID NO 9; 205pp; English.
 09-JUL-2003; 2003WO-US021703.
 12-JUL-2002; 2002US-0395402P.
 ۵,
 Best Local Similarity 100.
Matches 383; Conservative
 Wang J, Zhou
 2004-122914/12.
 (NUVE-) NUVELO INC
 N-PSDB; ADO47891
 Sequence 416 AA;
 WO2004007672-A2
 Homo sapiens
 22-JAN-2004.
 61
 121
 Query Match
 Rupp F,
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ADO47892 standard; protein; 416 AA

ADO47892 ID ADO

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121
 181
 334
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 361
 ABG75378;
 Мив вр.
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 The invention relates to a novel isolated polynucleotide and the encoded polypeptide. The molecules of the invention demonstrate antinflammatory, neuroprotective, antianaemic, cyrostatic and vulnerary activities and may be useful in preparing a composition for diagnosing or treating inflammatory, haematopoietic, immune, neurodegenerative or stem cell disorders, such as aplastic anaemia or cancer, as well as for promoting wound healing. The molecules may also be utilised during gene therapy procedures. The current sequence is that of a human therapeutic protein of the invention. The current sequence is not shown explicitly within the specification but can be accessed from the WIPO web-site.
 LYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACWKPSKRKQKKL 273
 EKQNSLEYMDQNDDRLKPEADTLPRSGEQERKNPMALYILKDKDSPETEENPAPEPRSAT 333
 EPGPPGYSVSPAVPGRSPGLPIRSARRYPRSPARSPATGRTHSSPPRAPSSPGRSRSASR 360
 Ma Y;
i G, Zhou P;
 or
 antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary; inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell; aplastic anaemia; cancer; wound healing; gene therapy.
 EKQNSLEYMDQNDDRLKPEADTLPRSGEQERKNPMALYILKDKDSPETEENPAPEPRSAT
 New polynuclectide, useful in preparing a composition for diagnosing treating inflammatory, neurodegenerative or stem cell disorders, e.g. aplastic anemia or cancer for promoting wound healing.
 Query Match 100.0%; Score 1962; DB 8; Length 416; Best Local Similarity 100.0%; Pred. No. 3e-134; Matches 383; Conservative 0; Mismatches 0; Indels 0;
 Z, M
Weng
 Zhang J, Wehrman T, Wang
Wang J, Ghosh M, Xue AJ,
 Claim 20; SEQ ID NO 1293; 718pp; English.
 Human therapeutic protein - SEQ ID 1293
 TLRTAGVHIIREQDEAGPVEISA 383
 Ā
 ADS11056 standard; protein; 416
 30-SEP-2003; 2003WO-US030720.
 2002US-0416186P.
 Ren F,
 Zhao QA,
 (first entry)
 Asundi V,
 WPI; 2004-668857/65.
 (NUVE-) NUVELO INC.
 Chen R,
 N-PSDB; ADS10372.
 Sequence 416 AA;
 WO2004080148-A2.
 Homo sapiens
 02-OCT-2002;
 16-DEC-2004
 23-SEP-2004.
 Tang YT,
Wang D, C
 ADS11056;
 334
 214
 274
 361
 241
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Gaps

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213
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 273
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 The present invention provides the protein and coding sequences of a novel human immunoglobulin domain-containing cell surface recognition molecule known as INSP052. The polypeptide is useful as immunoglobulin domain-containing cell surface recognition molecule. The sequences may also be used in therapy or diagnosing a disease or in the manufacture of a medicament for treating a disease. The disease is a cell proliferative,
120
 153
 STIVLELSEAFILNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 393
 New INSPOS2 polypeptides and nucleic acids, useful in diagnosing and treating cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, psychiatric, developmental, genetic or metabolic disorder.
 214 LYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACWKPSKRKQKKL
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA
 94 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA
 LYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACWKPSKRKQKKL
 EKONSLEYMDONDDRLKPEADTLPRSGEQERKNPMALYILKDKDSPETERNPAPEPRSAT
 INSP052; human; cell proliferation; autoimmune disease; inflammation; cardiovascular disease; neurological disease; psychiatric disease; developmental disease; metabolic disorder; infection; immunoglobulin domain-containing cell surface recognition molecule.
 ပ်
 Power
 383
 Š
 Phelps CB,
 Example 1; Page 68; Opp; English.
 TLRTAGVHIIREODEAGPVEISA
 Murine INSP052 complete protein.
 ABG75378 standard; protein; 418
 30-APR-2002; 2002GB-00009884.
 30-APR-2003; 2003WO-GB001851
 (first entry)
 (ARES-) ARES TRADING SA.
 Fagan RJ,
 WPI; 2003-903655/82.
 N-PSDB; ACH01276
 WO2003093316-A2.
 22-APR-2004
 Davids AR,
 13-NOV-2003
 241
 301
 394
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N-PSDB; ADQ63169
 sapiens
 30-OCT-2002
 AAE14784;
 61
 Query Match
 94
 121
 181
 241
 274
 328
 Peptide
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 273
 298
 ATEPGPPGYSVSPAVPGRSPGLPIRSARRYPRSPARSPATGRTHSSPPRAPSSPGRSRSA 358
 osteopathic, neuroprotective; nootropic; antiparkinsonian; cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
 213
 333
autoimmune/inflammatory, cardiovascular, neurological, psychiatric, developmental, genetic or metabolic disorder, an infection or other pathological condition. The polypeptides and nucleic acids are essential to the structural integrity and homeostatic functioning of most tissues. The present sequence is a polypeptide shown in the invention
 9
 93
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEXTINLTVDVPISRPQVLVA
 STIVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD
 KLEKQNSLEYMDQNDDRLKSEADTLPRSGEQERKNPMALYILKDKDSSEPDENPATEPRS
 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 VNITSPVRLIHGTVGKSALLSVQYSSTSSDKPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 STIVLELSEAFILNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD
 LYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACWKPSK--RKQK
 LYSCVVENPISQVRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACWKPSKKSRKKR
 KLEKONSLEYMDONDDRLKPEADTLPRSGEQERKNPMALYILKDKDSPETEENPAPEPRS
 Gaps
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 Ishii
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7
 Length 418;
 Sato H,
 10; Indels
 Query Match 94.3%; Score 1850; DB 7;
Best Local Similarity 94.5%; Pred. No. 4.2e-126;
Matches 364; Conservative 9; Mismatches 10;
 Wakamatsu A,
 Otsuki T, Waxu... r. Irie R;
 SRTLRTAGVHIIREQDEAGPVEISA 383
 ||:|||||||
SRSLRTAGVQRIREQDESGQVEISA 418
 Ş
 Novel human protein sequence #330.
 Nagai K,
 2003JP-00102206.
2003JP-00131392.
 21-JAN-2004; 2004EP-00001196
 ADQ65357 standard; protein;
 (first entry)
 Sugiyama T,
 Isono Y,
 WPI; 2004-535376/52
 Sequence 418 AA;
 EP1440981-A2.
 Homo sapiens
 21-JAN-2003;
 09-MAY-2003;
 Yamamoto J,
 07-OCT-2004
 28-JUL-2004
 Isogai T,
 Н
 61
 94
 154
 274
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 334
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 121
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The invention relates to 2495 novel polynucleotides (I) and their encoded polypeptides, sequences hybridizing to these nucleotides, sequences encoding partial polypeptides and sequences having 70% or 90% identity to the nucleotide and protein sequences. The nucleotides and polypeptides are useful as diagnostic markers or therapeutic target for the diseases or morpid states. They are also useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers. This sequence corresponds to a protein sequence of the invention.
 120
 153
 273
 290
 180
 213
 240
 Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers
 9
 93
 154 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRWLLSPDQKVLTITRVLMEDDD
 34 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA
 214 LYSCVVENPISOGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACWKPSKRKQKKL
 EKONSLEYMDONDDRLKPEADTLPRSGEQERKNPMALYI------LKDKDSPETEE
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 STIVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD
 LYSCMVENPISOGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACWKPSKRKOKKL
 Gaps
 Human; immunoglobulin superfamily protein-4; IGSFP-4; asthma; immune system disorder; acquired immune deficiency syndrome; AIDS; atherosclerosis; neurological disorder; Alzheimer's disease; Parkinson's disease; developmental disorder; renal tubular acidosis;
 17;
 8; Length 367;
 anaemia; muscle disorder; cardiomyopathy; myocarditis; cancer;
 Indels
 cell proliferative disorder; arteriosclerosis; hepatitis
 Human immunoglobulin superfamily protein (IGSFP)-4.
 67.2%; Score 1318.5; DB 8; 83.2%; Pred. No. 1.7e-87; ive 12; Mismatches 26;
 Claim 1; SEQ ID NO 2518; 2449pp; English.
 316
 354
 34. .298 _____/
/note= "Mature IGSFP-4"
43. .231
 1. .33
/label= Signal_peptide
 291 NPAPEPRS-ATEPGPPGYSVSPAVPGR
 LPSDLGASKGKEPEPASLASSHSLPRR
 Location/Qualifiers
 Z
 AAE14784 standard; protein; 298
 (first entry)
 Best Local Similarity 83.2
Matches 272; Conservative
 Sequence 367 AA;
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241 EKQNSLEYMDQNDDRLKP

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The present sequence is human immunoglobulin superfamily protein (IGSFP)-

4. The IGSFP polypeptide and polymucleotide are useful for diagnosing,

4. The IGSFP polypeptide and polymucleotide are useful for diagnosing,

5. Treating or preventing disorders associated with aberrant expression of

6. IGSFP e.g. immune system disorders (e.g. acquired immune deficiency

8. Syndrome (AIDS), asthma, atherosclerosis, psoriasis, uveitis),

7. neurological disorders (e.g. Alzheimer's disease, Huntington's disease,

7. dementia, Parkinson's disease), Alzheimer's disease, Huntington's disease,

7. dementia, Parkinson's disease), anaemia), muscle disorders (e.g. renal

7. cardiowypathy, mycarditis), or cell proliferative disorders (e.g.

7. cardiowypathy, mycarditis), or cell proliferative disorders (e.g.

7. cardiowypathy, mycarditis, and cancer). The polypeptide and

8. polymucleotide are also useful for assessing the effects of excenous

8. compounds on their expression. The polypeptide is useful in drug

8. compounds on their expression. The polymucleotide is useful for creating

8. selements on a microarray. The polymucleotide is useful for creating

8. knock-in humanised animals or transgenic animals to model human diseases,

8. in somatic or germline gene therapy, to generate a transcript image of a

8. compounds of the compound of the compounds of a compound of the compounds

8. compounds of the compounds of the compounds

9. compounds on their expression of the compounds

9. compounds on their expression of the chromosomal
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 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 60
 34 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 93
 Novel human immunoglobulin superfamily polypeptide, useful in diagnosis, prevention or treatment of immune system, neurological, developmental, muscle and cell proliferative disorders.
 location due to translocation, inversion among normal, carrier or affected individuals, and as hybridisation probes for mapping naturally
 Gaps
/note= "Antigen precursor signal immunoglobulin fold glycoprotein T cell surface transmembrane"
 Thangavelu K, Ramkumar J;
Arvizu C, Yao MG;
 ö
 66.9%; Score 1312; DB 5; Length 298; 100.0%; Pred. No. 3.7e-87;
 0; Indels
 161. .219
/label= Immunoglobulin_domain
243. .263
 /label= Immunoglobulin_domain
 /label= Transmembrane domain
 100.0%; Pred.
 Elliott VS,
Gandhi AR,
 Claim 1; Page 109-110; 122pp; English
 15-NOV-2001; 2001WO-US044974
 16-NOV-2000; 2000US-0249645P
 (INCY-) INCYTE GENOMICS INC
 Lu DAM, Yue H,
 occurring genomic sequences
 258; Conservative
 2002-519384/55.
 Similarity
 N-PSDB; AAD36780.
 Sequence 298 AA;
 WO200240671-A2
 Lo TP,
 Baughn MR,
 61
 94
 121
 181
 Query Match
 Local
 Domain
 Domain
 Domain
 Matches
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New isolated polypeptides and polynucleotides useful in diagnostics, forensics, in preventing or treating diseases such as HIV and cancer, and as drug targets.
 The invention relates to novel isolated polynucleotides and polypeptides encoded by them. Also included are mutants or variants of the polynucleotides and polypeptides. A polypeptide of the invention has virucide, anti-HTV, cytostatic, antiinflammatory, antiallargic, immunosuppressive, antiarteriosclerotic, hypotensive, osteopathic, hamitanemic, neuroprotective, noctropic, antianterioscipic, antiantesthanic, antiantesthanic, antidiabetic, and cardiant activity. The composition and methods are useful in diagnostics, forensics, gene or chromosome mapping, identification of mutantions responsible for genetic disorders or other traits, in assessing biodiversity, or in producing many other types of data and products dependent on DNA and amino acid sequences. They may in the composition and activities of data and products dependent on DNA and amino acid sequences.
 also be used in preventing or treating diseases (e.g. HIV and other viral infections, cancer, inflammation, allergies, graft rejection, atherosclerosis, hypertension, osteoporosis, anaemia, Alzheimer, addisease, Parkinson's disease, asthma, diabetes, myocardial infarction or haemophilia). They may also be used as targets in drug screening. The present sequence represents a polypeptide of the invention.
 immunosuppressive; antiarteriosclerotic; hypotensive; osteopathic; antianaemic; neuroprotective; nootropic; antiparkinsonian; antiasthmatic; haemostatic; antidiabetic; cardiant; HIV; viral infection; cancer; inflammation; allergy; graft rejection; atherosclerosis; hypertension; osteoporosis; anaemia; Alzheimer's disease; Parkinson's disease; asthma; diabetes; myocardial infarction; haemophilia.
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 60
 human; virucide; anti-HIV; cytostatic; antiinflammatory; antiallergic;
 Gaps
 .;
0
 Indels
 Tang YT;
 60.8%; Score 1192; DB 8;
100.0%; Pred. No. 1.5e-78;
iive 0; Mismatches 0;
 Wang ZW,
 Wehrman T,
 Claim 10; SEQ ID NO 7; 205pp; English.
 ADO47890 standard; protein; 237 AA.
 Human mature protein SEQ ID NO:7.
 291
 09-JUL-2003; 2003WO-US021703.
 12-JUL-2002; 2002US-0395402P.
Ъ,
 (first entry)
 Conservative
 Wang J, Zhou
 WPI; 2004-122914/12.
N-PSDB; ADO47888.
 Local Similarity
 (NUVE-) NUVELO INC
 Sequence 237 AA;
 WO2004007672-A2.
 Homo sapiens.
 15-JUL-2004
 22-JAN-2004
 235;
 ADO47890;
 Query Match
 Rupp F,
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Matches
 ADO47890
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Gaps

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Length 270; Indels

60.8%; Score 1192; DB 8; 100.0%; Pred. No. 1.8e-78; ive 0; Mismatches 0;

Conservative

Local Similarity es 235; Conserv

Matches

Query Match

Sequence 270 AA;

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The invention relates to novel isolated polynucleotides and polypeptides encoded by them. Also included are mutants or variants of the encoded by them. Also included are mutants or variants of the polynucleotides and polypeptides. A polypeptide of the invention has virucide, anti-HIV, cytostatic, antiinflammatory, antiallargic, immunosuppressive, artiarteriosclarctic, hypotensive, osteopathic, antiandamentic, neuroprotective, nootropic, antiantarkinatic, natiantaliabetic, and cardiant activity. The composition and methods are useful in diagnostics, forensics, gene or chromosome mapping, identification of mutations responsible for genetic disorders or other traits, in assessing biodiversity, or in producing many other types of data and producte dependent on DNA and amino acid sequences. They may also be used in preventing or treating diseases (e.g. HIV and other viral infections, cancer, inflammation, allergies, graft rejection, atherosclerosis, hypertension, osteoporosis, anaemia, Alzheimer's disease, parkinson's disease, asthma, diabetes, myocardial infarction or haemophila). They may also be used as targets in drug screening. The present sequence represents a polypeptide of the invention.
 120
 New isolated polypeptides and polynucleotides useful in diagnostics, forensics, in preventing or treating diseases such as HIV and cancer, and as drug targets.
 immunosuppressive; antiarteriosclerotic; hypotensive; osteopathic; antianaemic; neuroprotective; nootropic; antiparkinsonian; antiasthmatic; haemostatic; antidiabetic; cardiant; HIV; viral infection; cancer; inflammation; allergy; graft rejection; atherosclerosis; hypertension; osteoporosis; anaemia; Alzheimer's disease; Parkinson's disease; asthma; diabetes; myocardial infarction; haemophilia.
 9
 human; virucide; anti-HIV; cytostatic; antiinflammatory; antiallergic;
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA
 STIVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD
VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 STIVLELSEAFILNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD
 235
 LYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACWKPSKR
 Tang YT;
 Wang ZW,
 Wehrman T,
 Claim 10; SEQ ID NO 4; 205pp; English.
 ADO47887 standard; protein; 270 AA
 09-JUL-2003; 2003WO-US021703.
 12-JUL-2002; 2002US-0395402P.
 (first entry)
 Human protein SEQ ID NO:4.
 ъ,
 Zhou
 WPI; 2004-122914/12.
 (NUVE-) NUVELO INC
 Rupp F, Wang J,
 N-PSDB; ADO47886.
 WO2004007672-A2
 Homo sapiens.
 15-JUL-2004
 22-JAN-2004.
 121
 ADO47887;
 Н
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 181
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213
 120
 153
 180
 The invention relates to a novel isolated polynucleotide and the encoded polypeptide. The molecules of the invention demonstrate antinflammatory, be useropicetive, antianaemic, cytostatic and vulnerary activities and may be useful in preparing a composition for diagnosing or treating inflammatory, haematopoietic, immune, neurodegenerative or stem cell disorders, such as aplastic anaemia or cancer, as well as for promoting wound healing. The molecules may also be utilised during gene therapy procedures. The current sequence is that of a human therapeutic protein of the invention. The current sequence is not shown explicitly within the specification but can be accessed from the WIPO web-site.
 Y;
 9
 93
 or
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVFISRPQVLVA
 154 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD
 antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary; inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell; aplastic anaemia; cancer; wound healing; gene therapy.
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA
 STIVLELSEAFILNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD
1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 34 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 235
 New polynucleotide, useful in preparing a composition for diagnosing treating inflammatory, neurodegenerative or stem cell disorders, e.g. aplastic anemia or cancer for promoting wound healing.
 LYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACWKPSKR
 Ma
G
 Z, M
Weng
 Zhang J, Wehrman T, Wang Wang J, Ghosh M, Xue AJ,
 Claim 20; SEQ ID NO 1292; 718pp; English
 Human therapeutic protein - SEQ ID 1292.
 ADS11055 standard; protein; 270 AA.
 30-SEP-2003; 2003WO-US030720.
 02-OCT-2002; 2002US-0416186P
 Ren F,
 Asundi V, Ren F,
Chen R, Zhao QA,
 (first entry)
 WPI; 2004-668857/65.
N-PSDB; ADS10371.
 (NUVE-) NUVELO INC.
 WO2004080148-A2
 Homo saptens
 16-DEC-2004
 23-SEP-2004
 61
 94
 121
 181
 ADS11055;
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 Tang YT,
Wang D,
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LKDKDSPETEENPAPEPRSATEPGPPGYSVSPAVPGRSPGLPIRSARRYPRSPARSPATG 339
 The present invention relates to novel human transmembrane proteins (TMP) and polynucleotides encoding such proteins. Sequences of the invention are useful for treating diseases or conditions associated with abnormal expression of TMP such as discorders of reproduction (e.g. infertility, prostatitis), developmental (e.g. anaemia, epilepsy), gastrointestinal (e.g. anorexia, Crohn's disease), neurological (e.g. Alzhaimer's disease, stroke), lipid metabolism (e.g. hypercholesterolaemia, hyperlipidaemia), cardiovascular (e.g. atherosclerosis, hypertension), cell proliferative (e.g. cancer, psoriasis) and autoimmune disorders (e.g. acquired immune deficiency syndrome (AIDS), gout, Grave's disease). They are useful for creating knockout humanised animals or transgenic animals to model human disease. Sequences of the invention are also used in gene therapy. The present sequence is TMP-7 protein
 1 MLLSPDQKVLTITRVLMEDDDLYSCAVENPISQGRSLPVKITVYRRSSLYIILSTGGIFL
 160 MLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFL
 LVTLVTVCACWKPSKRKQKKLEKQNSLEYMDQNDDRLKPEADTLPRSGEQERKNPMALYI
 INSP052; human; cell proliferation; autoimmune disease; inflammation; cardiovascular disease; neurological disease; psychiatric disease; developmental disease; metabolic disorder; infection; immunoglobulin domain-containing cell surface recognition molecule.
 Gaps
 ;
0
anorexia, hypercholesterolemia, cancer, gout, Grave's disease
 Length 224;
 RTHSSPPRAPSSPGRSRSASRTLRTAGVHIIREQDEAGPVEISA 383
 Indels
 .
0
 Query Match
59.0%; Score 1157; DB 5;
Best Local Similarity 100.0%; Pred. No. 4.9e-76;
Matches 224; Conservative 0; Mismatches 0;
 Power C;
 Page 132-133; 163pp; English
 INSP052 extracellular domain protein.
 Ā
 Phelps CB,
 ABG75380 standard; protein; 246
 30-APR-2003; 2003WO-GB001851
 30-APR-2002; 2002GB-0009884
 (first entry)
 (ARES-) ARES TRADING SA.
 Fagan RJ,
 WPI; 2003-903655/82.
N-PSDB; ACH01279.
 Sequence 224 AA;
 WO2003093316-A2
 Unidentified
 22-APR-2004
 13-NOV-2003
 Davids AR,
 Claim 62;
 220
 280
 340
 181
 ABG75380;
 RESULT 13
 ABG75380
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 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 153
 213
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 9
 93
 Human; transmembrane protein; TMP-7; developmental disorder; epilepsy; prostatitis; infertility; neurological disorder; Alzheimer's disease; anamemia; stroke; cardiovascular disorder; hypertension; atherosclerosis; gastrointestinal disorder; anorexia; Crohn's disease; lipid metabolism; hypercholesterolaemia; hyperlipidaemia; cell proliferative disorder; psoriasis; autoimmune disorder; acquired immune deficiency syndrome; AlDS; cancer; gout; Grave's disease; transgenic; transgenic animal; gene therapy; antiinfertility; anticonvalsant; hypotensive; nootropic; neuroprotective; cerebroprotective; antiinflammatory; cytostatic;
 Burford N, Gandhi AR, Walia NK;
BM, Baughn MR, Lee EA, Khan FA;
PG, Thangavelu K, Ramkumar J;
 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 Novel human transmembrane proteins and polynucleotides useful for diagnosing, treating or preventing infertility, anemia, hypertension,
 Gaps
 LYSCMVENPISOGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACWKPSKR 235
 ö
 Length 270;
 Indels
 ..
0
 60.8%; Score 1192; DB 8; 100.0%; Pred. No. 1.8e-78;
 "Transmembrane domain"
 Human transmembrane protein (TMP)-7 protein.
 100.0%; Preu. ...
 Batra S,
Duggan Br
Lal F
 Location/Qualifiers
 AAE26421 standard; protein; 224 AA
 DAM, Duc
Yao MG,
 Au-Young J;
 2000US-0244017P.
2000US-0252855P.
2000US-0251825P.
 12-DEC-2000; 2000US-0255085P.
 2001WO-US049670
 (INCY-) INCYTE GENOMICS INC.
 (first entry)
 Yue H,
 Xu Y, Yue H,
Tang YT, Lu D
Azimzai Y, Y
 Matches 235; Conservative
 /note=
 2002-463354/49.
 Similarity
 Nguyen DB, Azimza
Tran B, Ding L,
 N-PSDB; AAD44098
 Sequence 270 AA;
 WO200234783-A2
 27-OCT-2000; 22-NOV-2000; 2
 26-OCT-2001;
 sapiens
 13-DEC-2002
 antithyroid
 02-MAY-2002
 Warren BA,
 Arvizu C,
 AAE26421;
 61
 94
 121
 154
 181
 214
 Query Match
 Local
 Domain
 Homo
 RESULT 12
 AAE2642
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ö 219

279

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The present invention provides the protein and coding sequences of a novel human immunoglobulin domain-containing cell surface recognition molecule known as INSPOS2. The polypeptide is useful as immunoglobulin domain-containing cell surface recognition molecule. The sequences may also be used in therapy or diagnosing a disease or in the manufacture of a medicament for treating a disease. The disease or in the manufacture of autoimmune/inflammatory, cardiovascular, neurological, psychiatric, pathological condition. The polypeptides and nucleic acids are essential to the structural integrity and homeostatic functioning of most tissues. The present sequence is a polypeptide shown in the invention
New INSP052 polypeptides and nucleic acids, useful in diagnosing and treating cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, psychiatric, developmental, genetic or metabolic disorder.
 Claim 1; Fig 7; Opp; English.
 Sequence 246 AA;
```

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ö
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 STIVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 93
 34 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWOLKRDKPVTVVOSIGTEVIGTLRP
 Gaps
 ö
 Length 246;
 0; Indels
Score 1045; DB 7;
Pred. No. 7.7e-68;
0; Mismatches 0;
 214 LYSCMVENPISQGRSLPVKITVYRRSS 240
 181 LYSCMVENPISQGRSLPVKITVYRRSS 207
 53.3%; 1
 Matches 207; Conservative
Query Match.
Best Local Similarity
 61
 94
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ADM87341 standard; protein; 256 AA Human protein SEQ ID NO:434. (first entry) 03-JUN-2004 ADM87341; 

gastrointestinal; antibacterial; immunosuppressive; antidiabetic; antirheumatic; gene therapy; molecular weight marker; chromosome marker; chromosome tag; genetic fingerprinting; nutritional supplement; cancer; inflammatory condition; arthritis; inflammatory bowel disease; chroh's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1; graft versus host disease; human. respiratory; cytostatic; antiarthritic; antiinflammatory;

Homo sapiens

WO2004009834-A2.

29-JAN-2004.

19-JUL-2002; 2002WO-US022858

21-JUL-2001; 2001US-0306971P. 28-MAR-2002; 2002US-00112944.

(NUVE-) NUVELO INC.

Wang J; Xue A, Ren F, Zhang J, Tang YT, Yang Y, Weng G,

The present invention describes an isolated polynucleotide (I): (a) which encodes a polypeptide with biological activity, where the which encodes a polypeptide equence selected from SEQ ID Noil-144; or (b) which encodes a polypeptide with biological activity, where the polynucleotide hybridises to (I) under stringent hybridisation conditions or reasons as greater than 99 as sequence identity with (I). (I) has respiratory, cytostatic, antiatrhitic, antidinflammatory, astrointestinal, antiatrhitic, antidinflammatory, astrointestinal, antiatrhitic, antidinflammatory astrointestinal, antidiates and can be used antichemmatic activity protein sequences in gene therrapy. (I) can be used for generating polynucleotides encoding chimeric or fusion proteins and can be used no express recombinant protein for analysis, characterisation or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags to identify chromosomes or to map related gene consummations or described propertions; to compare with endogenous DNA sequences in parients of consummations of an option of entire process of discovering other novel polynucleotides; for dentify potential genetic discovering other novel polynucleotides; for sequences in a source of information to derive for support, including for examination of expression patterns; to raise anti-one antibodies using DNA immunisation techniques; and as an antigen to raise anti-one antibodies using DNA immunisation and expression patterns; to raise anti-one source or as a source of carbohydrates. The polynucleotides and polypeptides can also be used treat cancer. The compositions are useful for promoting better or faster closure of non-healing wounds, for the generation and areament of fung or liver fibrosis, compositions are useful for promoting better or faster closure of non-healing wounds, for the generation and as an also be used treat cancer. Compositions are useful for promoting better New isolated polynucleotides and polypeptides, useful for treating, e.g. cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease, Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft Z, Q A English. Zhao Claim 20; SEQ ID NO 434; 591pp; ď Wang US patent US20040048249A1. Ghosh MJ, versus host disease. 2004-143291/14. Sequence 256 AA; Wehrman T, 

Gaps ; 0 52.4%; Score 1029; DB 8; Length 256; 96.2%; Pred. No. 1.2e-66; Indels 5; Mismatches Conservative Query Match Best Local Similarity Matches 203; Conserv

9 93 34 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP

DYRDRIRLFENGSLILSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120

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LYSCMVENPISQGRSLPVKITVYRRSSLYII 211 181

| ||:|||||:|||:||| || ||||||::|| ||| LDSCVVENPINQGRTLPCKITVYKKSSFYII

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STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITKVLMEDDD 180
 The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention
 61 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 94 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLGA 153
 Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomatc; morkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 60
 34 VNITSPVRLIHGINGHING SALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 93
 Gaps
 Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use.
 Chen R, Asundi V;
 ó
 51.9%; Score 1018; DB 4; Length 256; 96.6%; Pred. No. 7.5e-66; tive 4; Mismatches 3; Indels (
 Zhou P, Qian XB, Wang Z,
 Human EST encoded protein SEQ ID NO: 1763.
 Claim 20; Page 1159-1160; 1275pp; English.
 181 LYSCMVENPISQGRSLPVKITVYRRSSL 208
 AAM24238 standard; protein; 256 AA.
 25-JAN-2000; 2000US-00491404.
17-JUL-2000; 2000US-00617746.
03-AUG-2000; 2000US-00631451.
15-SEP-2000; 2000US-00631871.
 25-JAN-2001; 2001WO-US002687.
 (first entry)
 Query Match
Best Local Similarity 96.6
Matches 201; Conservative
 Tang YT, Liu C, Zh
Cao Y, Drmanac RA,
 WPI; 2001-476164/51.
N-PSDB; AAH98897.
 (HYSE-) HYSEQ INC
 Sequence 256 AA;
 WO200154477-A2.
 Homo sapiens.
 12-OCT-2001
 02-AUG-2001.
 AAM24238;
 121
 154
RESULT 15
AAM24238
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Search completed: July 26, 2005, 16:07:36 Job time : 110.756 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein July 26, 2005, 15:54:21 ; Search time 58.6445 Seconds Run on:

(without alignments)
1365.166 Million cell updates/sec

US-10-706-691-22 Perfect score: Title:

1 VNITSPVRLIHGTVGKSALL.......NPISQGRSLPVKITVYRRSS 207 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2105692 Total number of hits satisfying chosen parameters: 2105692 seqs, 386760381 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* A\_Geneseq\_16Dec04:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\*geneseqp2001s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp20048:\*

## SUMMARIES

|               |       |                |        |     | SOUTHFREE |              |           |
|---------------|-------|----------------|--------|-----|-----------|--------------|-----------|
|               |       | do             |        |     |           |              |           |
| Result<br>No. | Score | Query<br>Match | Length | DB  | ,<br>OI   | Description  |           |
| -             | 1045  | 100.0          | 237    | . 8 | ADO47890  | Ado47890 Hun | Human mat |
| 7             | 1045  | 100.0          | 246    | 7   | ABG75380  |              | INSP052 e |
| 3             | 1045  | 100.0          | 270    | 80  | ADO47887  |              | Human pro |
| 4             | 1045  | 100.0          | 270    | œ   | ADS11055  |              | Human the |
| S             | 1045  | 100.0          | 298    | ß   | AAE14784  | Aae14784 Hun | Human imm |
| 9             | 1045  | 100.0          | 383    | œ   | ADO47895  | Ado47895 Hun | Human mat |
| 7             | 1045  | 100.0          |        | 7   | ABG75379  | Abg75379 Pre | Predicted |
| 80            | 1045  | 100.0          |        | 7   | ABG75377  |              | Human INS |
| σ             | 1045  | 100.0          | 416    | œ   | ADO47892  | ~            | Human pro |
| 10            | 1045  | 100.0          |        | œ   | ADS11056  | _            |           |
| 11            | 1032  | 98.8           |        | œ   | ADQ65357  |              | Novel hum |
| 12            | 1029  | 98.5           |        | 7   | ABG75378  | _            | Murine IN |
| 13            | 1014  | 97.0           | 256    | 4   | AAM24238  | _            | Human EST |
| 14            | 1014  | 97.0           | 256    | 8   | ADM87341  | Adm87341 Hun | Human pro |
| 15            | 1014  | 97.0           | 256    | œ   | ADM87787  | Adm87787 Hun |           |
| 16            | 1014  | 97.0           | 256    | œ   | ADS12269  | Ads12269 Hun | Human the |
| 17            | 1014  | 97.0           | 256    | æ   | ADS12268  | _            | Human the |
| 18            | 548   | 52.4           |        | 7   | ABG75371  | Ξ.           | Human INS |
| 19            | 484   | 46.3           |        | 7   | ABG75372  | Abg75372 Hun | Human INS |
| 20            | 268   | 25.6           | 338    | 4   | AAM78339  | Ξ            | Human pro |
| 21            | 268   | 25.6           | 450    | ~   | AAY13398  | Aay13398 Ami | Amino aci |
| 22            | 268   | 25.6           | 450    | m   | ADC78632  | _            | Human PRO |
| 23            | 268   | 25.6           | 450    | 4   | AAB80266  | Aab80266 Hur | Human PRO |
| 24            | 268   | 25.6           | 450    | 4   | AAU12360  | Aau12360 Hun | Human PRO |
| 25            | 268   | 25.6           | 450    | 'n  | AAU81958  | Aau81958 Hun | Human PRO |

| Abu71644 Human PRO Abo17804 Novel hum Abu71499 Human PRO Abu81.058 Human Rec Abo11828 Novel hum Abu66758 Human Rec Abo5788 Human PRO Abu5983 Novel hum Abu67416 Human Rec Abo47416 Human Rec Abu5983 Novel sec Abu5983 Novel sec Abu64753 Human Rec Abu64753 Human Rec Abu64753 Human Rec Abu64753 Human Rec Abu64553 Human Rec Abu64563 Human Rec Abu64563 Human Rec Abu67034 Human Rec Abu67034 Human Rec | Human<br>Novel<br>Human                                            |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------|
| ABU71644 ABU71804 ABU81058 ABU81058 ABU81058 ABU61945 ABU61401 ABU64401 ABU6453 ABU625029 ABU6553 ABU64919 ABU14919 ABU14919                                                                                                                                                                                                                                                                                                                                                                                                  | ABO14858<br>ADA45897<br>ADA76328<br>ADB29524                       |
| , , , , , , , , , , , , , , , , , , ,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ουυυ                                                               |
| 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 4444<br>0004<br>0004                                               |
| 20000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                    |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 700<br>700<br>700<br>700<br>700<br>700<br>700<br>700<br>700<br>700 |
| 00000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | . 4 4 4 4<br>2 6 4 2                                               |

# ALIGNMENTS

human; virucide; anti-HIV; cytostatic; antiinflammatory; antiallergic; immunosuppressive; antiarteriosclerotic; hypotensive; osteopathic; antianaemic; neuroprotective; nootropic; antiparkinsonian; antiasthmatic; haemostatic; antidiabetic; cardiant; HIV; viral infection; cancer; inflammation; allergy; graft redjection; atherosclerosis; hypertension; osteoporosis; anaemia; Alzheimer's disease; Parkinson's disease; asthma; diabetes; myocardial infarction; haemophilia. ADO47890 standard; protein; 237 AA Human mature protein SEQ ID NO:7. (first entry) 15-JUL-2004 ADO47890; RESULT 1 ADO47890 

Homo sapiens

WO2004007672-A2.

22-JAN-2004.

09-JUL-2003; 2003WO-US021703.

12-JUL-2002; 2002US-0395402P.

(NUVE-) NUVELO INC.

Tang YT; Wang ZW, Wehrman T, Wang J, Zhou P, Rupp F,

WPI, 2004-122914/12.

N-PSDB; ADO47888

New isolated polypeptides and polynucleotides useful in diagnostics, forensics, in preventing or treating diseases such as HIV and cancer, and as drug targets.

Claim 10; SEQ ID NO 7; 205pp; English.

The invention relates to novel isolated polynucleotides and polypeptides encoded by them. Also included are mutants or variants of the polynuclectides and polypeptides. A polypeptide of the invention has virucide, anti-HIV, cytostatic, antiinflammatory, antiallergic, immunosuppressive, antiatratiosclerotic, antianaemic, neuroprotective, nootropic, antiparkinsonian, antiasthmatic, haemostatic, antidiabetic, and cardiant activity. The composition and

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ö
 identification of mutations responsible for genetic disorders or other traits, in assessing biodiversity, or in producing many other types of adara and products dependent on DNA and amino acid sequences. They may also be used in preventing or treating diseases (e.g. HIV and other viral infections, cancer, inflammation, allergies, graft rejection, atherosclerosis, hypertension, osteoporosis, anaemia, Alzheimer's disease, Parkinson's disease, asthma, diabetes, myocardial infarction or heemophilia). They may also be used as targets in drug screening. The present sequence represents a polypeptide of the invention.
 STIVLELSEAFILINCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 STIVLELSEAFILNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDOKVLTITRVLMEDDD 180
 9
 forensics, gene or chromosome mapping,
 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 Gaps
 ô
 Length 237;
 Indels
 100.0%; Score 1045; DB 8; 100.0%; Pred. No. 8.4e-83;
 ;
 0; Mismatches
 207
 LYSCMVENPISQGRSLPVKITVYRRSS
are useful in diagnostics,
 al Similarity 100.
207; Conservative
 Sequence 237 AA;
 121
 121
 181
 181
 Query Match
 nethods
 Local
 Matches
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INSP052 extracellular domain protein.
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 ABG75380 standard; protein; 246
 entry)
 (first
 ABG75380;
RESULT 2
 ABG75380
 CXSXGLAXBAXGXGXGXGXGXGXGXGXGXGXGXCCX
```

INSP052, human, cell proliferation; autoimmune disease, inflammation; cardiovascular disease, neurological disease; psychiatric disease; developmental disease; metabolic disorder; infection; infection; immunoglobulin domain-containing cell surface recognition molecule.

Unidentified

WO2003093316-A2 13-NOV-2003

30-APR-2003; 2003WO-GB001851

30-APR-2002; 2002GB-00009884

(ARES-) ARES TRADING SA.

GB, Phelps Davids AR, Fagan RJ,

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WPI; 2003-903655/82. N-PSDB; ACH01279. New INSP052 polypeptides and nucleic acids, useful in diagnosing and treating cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, psychiatric, developmental, genetic or metabolic disorder.

Claim 1; Fig 7; Opp; English.

ö present invention provides the protein and coding sequences The

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 120
 New isolated polypeptides and polynucleotides useful in diagnostics, forensics, in preventing or treating diseases such as HIV and cancer, and as drug targets.
 immunosuppressive, antiarteriosclerotic; hypotensive; osteopathic; antianaemic; neuroprotective; nootropic; antiparkinsonian; antiasthmatic; haemostatic; antidiabetic; cardiant; HIV; viral infection; cancer; inflammation; allergy; graft rejection; atherosclerosis; hypertension; osteoporosis; anaemia; Alzheimer's disease; Parkinson's disease; asthma; diabetes; myocardial infarction; haemophilia.
 94 DYRDRIRLFENGSLILSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 153
 molecule known as INSP052. The polypeptide is useful as immunoglobulin domain-containing cell surface recognition molecule. The sequences may also be used in therapy or diagnosing a disease or in the sequences may autoimmune/inflammatory, cardiovascular, neurological, psychiatric, developmental, genetic or metabolic disorder, an infection or other pathological condition. The polypeptides and nucleic acids are essential to the structural integrity and homeostatic functioning of most tissues. The present sequence is a polypeptide shown in the invention
 STIVLELSEAFILNCSHENGIKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 9
 34 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 93
 human; virucide; anti-HIV; cytostatic; antiinflammatory; antiallergic;
 DYRDRIRLFENGSLILSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 Gaps
 ö
 Length 246;
 YT;
 Indels
 Tang
 DB 7;
 ZW,
 ; Score 1045; DB 7;
; Pred. No. 8.8e-83;
0; Mismatches 0;
 Wang
 LYSCMVENPISOGRSLPVKITVYRRSS 207
 LYSCMVENPISQGRSLPVKITVYRRSS 240
 Wehrman T,
 ġ
 ADO47887 standard; protein; 270
 100.08;
 09-JUL-2003; 2003WO-US021703.
 12-JUL-2002; 2002US-0395402P.
 100.08;
 Д,
 Human protein SEQ ID NO:4.
 Local Similarity 100.
 Wang J, Zhou
 WPI; 2004-122914/12.
 (NUVE-) NUVELO INC.
 N-PSDB; ADO47886
 Sequence 246 AA;
 WO2004007672-A2
 Homo sapiens
 22-JAN-2004
 15-JUL-2004
 61
 121
 181
 ADO47887;
 Query Match
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 Matches
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 The invention relates to novel isolated polynucleotides and polypeptides encoded by them. Also included are mutants or variants of the concoded by them. Also included are mutants or variants of the polynucleotides and polypeptides. A polypeptide of the invention has virucide, anti-HIV, cytostatic, anti-All manatory, antial-Brgic, immunosuppressive, antiatratiosclerotic, hypotensive, osteopathic, antianaemic, neuroprotective, nootropic, antiparkinsonian, antiasthmatic, hartiansemic, neuroprotective, nootropic, antiparkinsonian, antiasthmatic, antidabetic, and cardiant activity. The composition and methods are useful in diagnostics, forensics, gene or chromosome mapping, identification of mutations responsible for genetic disorders or other traits, in assessing biodiversity, or in producing many other types of data and products dependent on DNA and amino acid sequences. They may also be used in preventing or treating diseases (e.g. HIV and other viral infections, cancer, inflammation, allergies, graft rejection, atherosclerosis, hypertension, osteoporosis, anemia, Alzheimer's diseases, Parkinson's disease, asthma, diabetes, myocardial infarction or haemophilia). They may also be used as targets in drug screening. The present sequence represents a polypeptide of the invention.
 ö
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 STIVLELSEAFTLNCSHENGTXPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 Ma Y;
Zhou P;
 93
 antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary; inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell; aplastic anaemia; cancer; wound healing; gene therapy.
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 Gaps
 Wang Z, Fr. Weng G,
 ö
 Length 270;
 Indels
 Wehrman T, Wang
hosh M, Xue AJ,
 100.0%; Score 1045; DB 8; 100.0%; Pred. No. 9.9e-83;
 Ghosh M,
 0; Mismatches
 LYSCMVENPISOGRSLPVKITVYRRSS 207
 214 LYSCMVENPISQGRSLPVKITVYRRSS 240
 Human therapeutic protein - SEQ ID 1292.
 Asundi V, Ren F, Zhang J,
Chen R, Zhao QA, Wang J, G
Claim 10; SEQ ID NO 4; 205pp; English.
 ADS11055 standard; protein; 270 AA.
 30-SEP-2003; 2003WO-US030720
 02-OCT-2002; 2002US-0416186P
 (first entry)
 Local Similarity 100.
nes 207; Conservative
 WPI; 2004-668857/65
 (NUVE-) NUVELO INC.
 Chen R,
 Sequence 270 AA;
 WO2004080148-A2.
 Homo sapiens
 16-DEC-2004
 23-SEP-2004.
 61
 94
 ADS11055;
 Query Match
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Matches
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The invention relates to a novel isolated polynucleotide and the encoded bolygeptide. The molecules of the invention demonstrate antiinflammatory, neuroprotective, antianaemic, cytostatic and vulnerary activities and may be useful in preparing a composition for diagnosing or treating inflammatory, haematopoletic, immune, neurodegenerative or stem cell disorders, such as aplastic anaemia or cancer, as well as for promoting wound healing. The molecules may also be utilised during gene therapy procedures. The current sequence is that of a human therapeutic protein of the invention. The current sequence is not shown explicitly within the specification but can be accessed from the WIPO web-site.
 180
 120
 94 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 153
 154 STITULELSEAFILNCSHENGTKPSYTWLKDGKPLLNDSRWLLSPDQKVLTITRVLMEDDD 213
 9
 93
 ö
 34 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA
 New polynucleotide, useful in preparing a composition for diagnosing treating inflammatory, neurodegenerative or stem cell disorders, e.g. aplastic anemia or cancer for promoting wound healing.
 Gapa
 Human; immunoglobulin superfamily protein-4; IGSFP-4; asthma; immune system disorder; acquired immune deficiency syndrome; AIDS; atherosclerosis; neurological disorder; Alzheimer's disease; Parkinson's disease; developmental disorder; renal tubular acidosis; anaemia; muscle disorder; cardiomyopathy; myocarditis; cancer; cell proliferative disorder; arteriosclerosis; hepatitis.
 /note= "Antigen precursor signal immunoglobulin fold glycoprotein T cell surface transmembrane"
 ;
0
 Length 270;
 Indels
 Human immunoglobulin superfamily protein (IGSFP)-4.
 100.0%; Score 1045; DB 8;
100.0%; Pred. No. 9.9e-83;
ive 0; Mismatches 0;
 /label= Immunoglobulin_domain
 161. .219
/label= Immunoglobulin_domain
 Claim 20; SEQ ID NO 1292; 718pp; English
 240
 181 LYSCMVENPISQGRSLPVKITVYRRSS 207
 /note= "Mature IGSFP-4"
 1. .33
/label= Signal_peptide
 LYSCMVENPISQGRSLPVKITVYRRSS
 Ą.
 Location/Qualifiers
 AAE14784 standard; protein; 298
 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 207; Conservative (
 (first entry)
 . .231
N-PSDB; ADS10371
 Sequence 270 AA;
 30-OCT-2002
 Homo sapiens
 AAE14784;
 121
 214
 Peptide
```

Human mature protein SEQ ID NO:12

(first entry)

15-JUL-2004

ADO47895;

```
The present sequence is human immunoglobulin superfamily protein (IGSFP)-

1. The IGSFP polypeptide and polynucleotide are useful for diagnosing,

2. treating or preventing disorders associated with aberrant expression of

2. IGSFP e.g. immune system disorders (e.g. acquired immune deficiency

3. Independent of the system disorders (e.g. acquired immune deficiency

3. Syndrome (AIDS), asthma, atherosolerosis, psoriasis, uvetis),

3. neurological disorders (e.g. Alzheimer's disease, Huntington's disease,

4. Cardiomyopathy, myocarditis), developmental disorders (e.g. renal

5. cardiomyopathy, myocarditis), or cell proliferative disorders (e.g.

5. cardiomyopathy, myocarditis), or cell proliferative disorders (e.g.

5. cardiomyopathy, myocarditis), or cell proliferative disorders (e.g.

5. cardiomyopathy, myocarditis), or cell proliferative disorders (e.g.

5. cardiomyopathy, myocarditis), or cell proliferative disorders (e.g.

5. cardiomyopathy, myocarditis), or cell proliferative disorders (e.g.

5. cardiomyopathy, myocarditis), or cell proliferative disorders (e.g.

5. cardiomyopathy, myocarditis, repetitis, and cancer). The polypeptide is useful in drug

5. cardiomyopathy, myocarding the proteome of a tissue or cell type,

6. cardiomyopathy, the polymucleotide is useful for creating

6. screening techniques, to analyse the proteome of a tissue or cell type,

7. snock-in humanised animals or transgenic animals to model human diseases,

7. in somatic or germline gene therapy, to generate a transcript image of a

7. tissue or cell type, for detecting differences in the chromosomal

7. location due to translocation, inversion among normal, carrier or

7. affected individuals, and as hybridisation probes for mapping naturally

7. creating genomic sequences
 ö
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 STIVLELSEAFTLNCSHENGTKPSYTWLKDGKPLINDSRWLLSPDGKVLTITRVLMEDDD 213
 34 VNITSPVRLIHGITUGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 93
 Novel human immunoglobulin superfamily polypeptide, useful in diagnosis, prevention or treatment of immune system, neurological, developmental, muscle and cell proliferative disorders.
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 60
 Gaps
 Elliott VS, Thangavelu K, Ramkumar J;
Gandhi AR, Arvizu C, Yao MG;
 ô
 Length 298;
 Indels
 100.0%; Score 1045; DB 5; 100.0%; Pred. No. 1.1e-82;
 ;
0
243. .263
/label= Transmembrane_domain
 0; Mismatches
 LYSCMVENPISQGRSLPVKITVYRRSS 207
 LYSCMVENPISOGRSLPVKITVYRRSS 240
 Claim 1, Page 109-110; 122pp; English
 15-NOV-2001; 2001WO-US044974.
 16-NOV-2000; 2000US-0249645P
 DAM, Yue H,
Gururajan R,
 (INCY-) INCYTE GENOMICS INC
 207; Conservative
 2002-519384/55
 Lu DAM,
 Similarity
 N-PSDB; AAD36780.
 Sequence 298 AA;
 WO200240671-A2.
 Lo TP,
 Baughn MR,
 61
 154
 121
 214
 Query Match
 181
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ADO47895 standard; protein; 383 AA

RESULT 6 AD047895

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The invention relates to novel isolated polynucleotides and polypeptides encoded by them. Also included are mutants or variants of the polynucleotides and polypeptides. A polypeptide of the invention has virucide, anti-HIV, cytostatic, antiinflammatory, antiallergic, immunosuppressive, antiaterriosclerctic, hypotensive, osteopathic, antialabetic, antidabetic, and cardiant activity. The composition and methods are useful in diagnostics, forensics, gene or chromosome mapping, identification of mutations responsible for genetic disorders or other traits, in assessing biodiversity, or in producing many other types of data and products dependent on DNA and amino acid sequences. They may also be used in preventing or treating diseases (e.g. HIV and other viral infections, cancer, inflammation, allergies, graft rejection, atherosclerosis, hypertension, osteoporosis, anaemia, Alzheimer's disease, Parkinson's disease, asthma, diabetes, myocardial infarction or haemophilia). They may also be used as targets in drug screening. The
 61 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRWLLSPDQKVLTITRVLMEDDD 180
 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITKVLMEDDD 180
 immunosuppressive, antiarteriosclerotic, hypotensive, osteopathic, antianaemic, neuroprotective, nootropic, antiparkinsonian; antiasthmatic; haemostatic, antidiabetic; cardiant, HIV, viral infection; cancer; inflammation; allergy; graft rejection; atherosclerosis; hypertension; osteoporosis; anaemia; Alzheimer's disease; Parkinson's disease; asthma; diabetes; myocardial infarction; haemophilia.
 New isolated polypeptides and polynucleotides useful in diagnostics, forensics, in preventing or treating diseases such as HIV and cancer, and
 9
 1 VNITSPVRLIHGIVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 human; virucide; anti-HIV; cytostatic; antiinflammatory; antiallergic;
 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 Gaps
 ..
 Length 383;
 Tang YT;
 Indels
 8
 .
 ; Score 1045; DB 8;
; Pred. No. 1.6e-82;
0; Mismatches 0;
 Wang ZW,
 Claim 10; SEQ ID NO 12; 205pp; English.
 Wehrman T,
 100.0%;
 09-JUL-2003; 2003WO-US021703
 12-JUL-2002; 2002US-0395402P
 ď
 Query Match
Best Local Similarity 100.
 Zhon
 WPI; 2004-122914/12.
 (NUVE-) NUVELO INC
 Rupp F, Wang J,
 drug targets.
 N-PSDB; ADO47893
 Sequence 383 AA;
 WO2004007672-A2
 Homo sapiens.
 22-JAN-2004
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2003-903655/82.
 WPI; 2003-903655/1
N-PSDB; ACH01275.
 Sequence 416 AA;
 WO2003093316-A2
 Homo sapiens.
 22-APR-2004
 Davids AR,
 181
 ABG75377;
 121
 Query Match
 RESULT 8
 ABG75377
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 The present invention provides the protein and coding sequences of a novel human immunoglobulin domain-containing cell surface recognition molecule known as INSP052. The polypeptide is useful as immunoglobulin domain-containing cell surface recognition molecule. The sequences may also be used in therapy or diagnosing a disease or in the manufacture of a medicament for treating a disease. The disease or in the manufacture of autoimmune/inflammatory, cardiovascular, neurological, psychiatric, developmental, genetic or metabolic disorder, an infection or other pathological condition. The polypeptides and nuclaic acids are essential to the structural integrity and homeostatic functioning of most tissues. The present sequence is a polypeptide shown in the invention
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 STIVLELSEAFTINCSHENGIKPSYIWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRWLLSPDQKVLTITRVLMEDDD 213
 93
 New INSP052 polypeptides and nucleic acids, useful in diagnosing and treating cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, psychiatric, developmental, genetic or metabolic disorder.
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 INSP052; human; cell proliferation; autoimmune disease; inflammation; cardiovascular disease; neurological disease; psychiatric disease; developmental disease; metabolic disorder; infection; immunoglobulin domain-containing cell surface recognition molecule.
 Gaps
 ö
 100.0%; Score 1045; DB 7; Length 416; 100.0%; Pred. No. 1.7e-82; ive 0; Mismatches 0; Indels 0
 ΰ
 Power
 LYSCMVENPISQGRSLPVKITVYRRSS 207
LYSCMVENPI SQGRSLPVKI TVYRRSS
 Phelps CB,
 Example 2; Fig 5; Opp; English
 30-APR-2003; 2003WO-GB001851
 30-APR-2002; 2002GB-00009884
 ABG75379 standard; protein;
 (first entry)
 Predicted INSP052 protein.
 Local Similarity 100.
1es 207; Conservative
 Davids AR, Fagan RJ,
 (ARES-) ARES TRADING
 WPI; 2003-903655/82.
N-PSDB; ACH01277.
 Sequence 416 AA;
 WO2003093316-A2.
 Unidentified
 22-APR-2004
 13-NOV-2003
181
 181
 61
 Query Match
 121
 Best Loca
Matches
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The present invention provides the protein and coding sequences of a novel human immunoglobulin domain-containing cell surface recognition molecule known as INSP052. The polypeptide is useful as immunoglobulin domain-containing cell surface recognition molecule. The sequences may also be used in therapy or diagnosing a disease or in the manufacture of a medicament for treating a disease. The disease or in the manufacture of autoimmune/inflammatory, cardiovascular, neurological, psychiatric, developmental, genetic or metabolic disorder, an infection or other pathological condition. The polypeptides and nucleic caids are essential to the structural integrity and homeostatic functioning of most tissues. The present sequence is a polypeptide shown in the invention
 61 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 213
 9
 93
 New INSP052 polypeptides and nucleic acids, useful in diagnosing and treating cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, psychiatric, developmental, genetic or metabolic disorder.
 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 VNITSPVRLIHGTVGKSALLSVOYSSTSSDRPVVKWOLKRDKPVTVVOSIGTEVIGTLRP
 INSP052; human; cell proliferation; autoimmune disease; inflammation;
 Gaps
 cardiovascular disease; neurological disease; psychiatric disease; developmental disease; metabolic disorder; infection; immunoglobulin domain-containing cell surface recognition molecule.
 ö
 Length 416;
 Indels
 100.0%; Score 1045; DB 7;
100.0%; Pred. No. 1.7e-82;
ive 0; Mismatches 0;
 ΰ
 Power
214 LYSCMVENPISQGRSLPVKITVYRRSS
 Ź
 Phelps CB,
 ABG75377 standard; protein; 416
 Human INSP052 complete protein.
 Claim 1; Page 67; Opp; English.
 30-APR-2003; 2003WO-GB001851.
 30-APR-2002; 2002GB-00009884
 Best Local Similarity 100. Matches 207; Conservative
 (ARES-) ARES TRADING SA
 Fagan RJ,
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DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120

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 The invention relates to novel isolated polynucleotides and polypeptides encoded by them. Also included are mutants or variants of the encoded by them. Also included are mutants or variants of the polynucleotides and polypeptides. A polypeptide of the invention has virucide, anti-HIV, cytostatic, antiinflammatory, antiallergic, antiantensmic, insurprotective, noctropic, antiparkinsonian, antiasthmatic, haemostatic, antidiabetic, and cardiant activity. The composition and methods are useful in diagnostics, forensics, genetic disorders or other traits, in assessing biodiversity, or in producing many other types of data and products dependent on DNA and amino acid sequences. They may also be used in preventing or treating diseases (e.g. HIV and other viral infections, cancer, inflammation, allergies, graft rejection, atherosclerosis, hypertension, osteoporosis, anemia, Alzheimer's disease, parkinson's disease, asthma, diabetes, myocardial infarction or haemophilial. They may also be used as targets in drug screening. The present sequence represents a polypeptide of the invention.
 human; virucide, anti-HIV; cytostatic; antiinflammatory; antiallergic; immunosuppressive, antiatreriosolerotic; hypotensive, osteopathic; antiatanemic; neuroprotective, nootropic; antiparkinsonian; antiasthmatic; haemostatic; antidiabetic; cardiant; HIV; viral infection; cancer; inflammation; allergy; graft rejection; atherosolerosis; hypertension; osteoporosis; anaemia; Alzheimer's disease; Parkinson's disease; asthma; diabetes; myocardial infarction; haemophilia.
 New isolated polypeptides and polynucleotides useful in diagnostics, forensics, in preventing or treating diseases such as HIV and cancer, and
 Length 416;
 Tang YT;
 100.0%; Score 1045; DB 8;
100.0%; Pred. No. 1.7e-82;
ive 0; Mismatches 0;
 Wang ZW,
207
 Wehrman T,
 Claim 10; SEQ ID NO 9; 205pp; English.
 214 LYSCMVENPISQGRSLPVKITVYRRSS
LYSCMVENPISQGRSLPVKITVYRRSS
 Ź
 ADO47892 standard; protein; 416
 09-JUL-2003; 2003WO-US021703.
 12-JUL-2002; 2002US-0395402P
 <u>م</u>
 (first entry)
 Human protein SEQ ID NO:9
 Zhou
 WPI; 2004-122914/12.
N-PSDB; ADO47891.
 Similarity
 (NUVE-) NUVELO INC
 Wang J,
 drug targets.
 Sequence 416 AA;
 MO2004007672-A2
 Homo sapiens
 22-JAN-2004.
 15-JUL-2004
 Query Match
181
 ADO47892;
 Rupp F,
 Local
 AD047893
 RESULT
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The invention relates to a novel isolated polynucleotide and the encoded polypeptide. The molecules of the invention demonstrate antiinflammatory, neuroprotective, antianaemic, cytostatic and vulnerary activities and may be useful in preparing a composition for diagnosing or treating inflammatory, haematopoletic, immune, neurodegenerative or stem cell disorders, such as aplastic anaemia or cancer, as well as for promoting wound healing. The molecules may also be utilised during gene therapy procedures. The current sequence is that of a human therapeutic protein of the invention. The current sequence is not shown explicitly within the specification but can be accessed from the WIPO web-site.
 Y;
Zhou P;
STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 213
 9
 34 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 93
 ö
 antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary; inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell; aplastic anaemia; cancer; wound healing; gene therapy.
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 New polynucleotide, useful in preparing a composition for diagnosing treating inflammatory, neurodegenerative or stem cell disorders, e.g. aplastic anemia or cancer for promoting wound healing.
 Gaps
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 Z, M
Weng
 Length 416;
 Indels
 Zhang J, Wehrman T, Wang
Wang J, Ghosh M, Xue AJ,
 100.0%; Score 1045; DB 8; 100.0%; Pred. No. 1.7e-82;
 ö
 0; Mismatches
 Claim 20; SEQ ID NO 1293; 718pp; English
 181 LYSCMVENPISQGRSLPVKITVYRRSS 207
 240
 Human therapeutic protein - SEQ ID 1293.
 LYSCMVENPISOGRSLPVKITVYRRSS
 ADS11056 standard; protein; 416 AA.
 30-SEP-2003; 2003WO-US030720.
 02-OCT-2002; 2002US-0416186P
 Ren F,
 Zhao QA,
 16-DEC-2004 (first entry)
 Conservative
 WPI; 2004-668857/65.
 sal Similarity
207; Conserva
 Asundi V,
 (NUVE-) NUVELO INC.
 Chen R,
 N-PSDB; ADS10372
 Sequence 416 AA;
 WO2004080148-A2.
 Homo sapiens,
 23-SEP-2004
 214
 ADS11056;
 121
 Tang YT,
 Query Match
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Matches
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Gaps

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Indels

Matches 207; Conservative

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34 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 93 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP

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The present invention provides the protein and coding sequences of a novel human immunoglobulin domain-containing cell surface recognition molecule known as INSPOS2. The polypeptide is useful as immunoglobulin domain-containing cell surface recognition molecule. The sequences may also be used in therapy or diagnosing a disease or in the manufacture of a medicament for treating a disease. The disease or in the manufacture of autoimmune/inflammatory, cardiovascular, neurological, psychiatric, developmental, genetic or metabolic disorder, an infection or other pathological condition. The polypeptides and nucleic acids are essential to the structural integrity and homeostatic functioning of most tissues. The present sequence is a polypeptide shown in the invention
 New INSP052 polypeptides and nucleic acids, useful in diagnosing and treating cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, psychiatric, developmental, genetic or metabolic disorder.
 STTVLELSEAFTLNCSHENGTKPSYTWLKOGKPLLNDSRMLLSPDQKVLTITRVLMEDDD
 VNITSPVRLIHGTVGKSALLSVQYSSTSSDKPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 INSP052; human; cell proliferation; autoimmune disease; inflammatic cardiovascular disease; neurological disease; psychiatric disease; developmental disease; metabolic disorder; infection; immunoglobulin domain-containing cell aurface recognition molecule.
 Score 1029; DB 7;
Pred. No. 4.3e-81;
2; Mismatches 1;
 ပ
 207
 Power
 LYSCVVENPISQGRSLPVKITVYRRSS
 LYSCMVENPISOGRSLPVKITVYRRSS
 Ź
 Phelps CB,
 Example 1; Page 68; Opp; English.
 Murine INSP052 complete protein.
 ABG75378 standard; protein; 418
 Query Match

Best Local Similarity 98.6%;
Matches 204; Conservative 2
 30-APR-2003; 2003WO-GB001851
 30-APR-2002; 2002GB-00009884
 (first entry)
 (ARES-) ARES TRADING SA
 Fagan RJ,
 WPI; 2003-903655/82.
N-PSDB; ACH01276.
 Sequence 418 AA;
 WO2003093316-A2
 22-APR-2004
 13-NOV-2003
 Davids AR,
 154
 94
 181
 214
 ABG75378;
 121
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 RESULT 12
 ABG75378
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 The invention relates to 2495 novel polynucleotides (I) and their encoded polypeptides, sequences hybridizing to these nucleotides, sequences encoding partial polypeptides and sequences having 70% to 90% identity to the nucleotide and protein sequences. The nucleotides and polypeptides are useful as diagnostic markers or therapeutic target for the diseases or morbid states. They are also useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers. This sequence corresponds to a protein
 213
 neuroprotective; nootropic; antiparkinsonian; cytostatic; diagnostic marker; morbid state; osteoporosis; disease; Alzheimer's disease; Parkinson's disease; dementia;
 Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA
 STIVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 Gaps
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 Ishii
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 DB 8; Length 367;
 Sato H,
 1; Indels
 Wakamatsu A,
 Score 1032; DB 8
Pred. No. 2e-81;
1; Mismatches
 Claim 1; SEQ ID NO 2518; 2449pp; English.
 Otsuki T, Wakami
Nagai K, Irie R;
 LYSCMVENPISQGRSLPVKITVYRRSS 207
 ADQ65357 standard; protein; 367 AA
 Novel human protein sequence #330,
 (REAS-) RES ASSOC BIOTECHNOLOGY
 21-JAN-2003; 2003JP-00102206.
09-MAY-2003; 2003JP-00131392.
 98.8%;
 21-JAN-2004; 2004EP-00001196
 Matches 205; Conservative
 Sugiyama T,
Isono Y,
 WPI; 2004-535376/52.
 Similarity
 N-PSDB; ADQ63169
 Sequence 367 AA;
 gene therapy;
neurological d
 Homo sapiens.
 osteopathic;
 EP1440981-A2.
 Yamamoto J,
 07-OCT-2004
 28-JUL-2004.
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[sogai T,

cancer

61 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120

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61 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120

VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 93

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sequence

Query Match

Local

9 93

Gaps

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Length 418; 1; Indels

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94 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLGA 153
 respiratory; cytostatic; antiarthritic; antiinflammatory; gastrointestinal; antibacterial; immunosuppressive; antidiabetic; antirheumatic; gene therapy; molecular weight marker; chromosome marker; chromosome tag; genetic fingerprinting; nutritional supplement; cancer; inflammatory condition; arthritis; inflammatory bowel disease; crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1; graft versus host disease; human.
 181 LYSCMVENPISQGRSLPVKITVYRRSS
 214 LYSCVVENPINGGRTLPCKITEYRKSS
 ADM87341 standard; protein; 256
 19-JUL-2002; 2002WO-US022858.
 21-JUL-2001; 2001US-0306971P.
28-MAR-2002; 2002US-00112944.
 Human protein SEQ ID NO:434.
 (first entry)
 Weng
 Ghosh MJ,
 WPI; 2004-143291/14.
 versus host disease.
 Yang Y,
 (NUVE-) NUVELO INC
 N-PSDB; ADM87097.
 WO2004009834-A2.
 Homo sapiens,
 03-JUN-2004
 29-JAN-2004
 Wehrman I,
 ADM87341;
 121
 Tang YT,
 RESULT 14
 ADM8734
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 Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a
 tags (ESTs)
 Gaps
 Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use.
 Asundi V;
 ö
 Score 1014; DB 4; Length 256;
Pred. No. 4.6e-80;
4; Mismatches 3; Indels (
 Chen R,
 7
 Human EST encoded protein SEQ ID NO: 1763.
 ou P, Qian XB, Wang
Zhang J, Werhman T;
 Claim 20; Page 1159-1160; 1275pp; English.
 207
 LYSCVVENPISOVRSLPVKITVYRRSS 240
 LYSCMVENPISQGRSLPVKITVYRRSS
 AAM24238 standard; protein; 256 AA
 25-JAN-2000; 2000US-00491404.
17-JUL-2000; 2000US-00617746.
03-AUG-2000; 2000US-00631451.
15-SEP-2000; 2000US-00663870.
 25-JAN-2001; 2001WO-US002687
 97.08;
 96.68;
 (first entry)
 Zhou P,
 Matches 200; Conservative
 the invention
 Tang YT, Liu C, Zh
Cao Y, Drmanac RA,
 2001-476164/51.
 Similarity
 (HYSE-) HYSEQ INC.
 Sequence 256 AA;
 N-PSDB; AAH98897
 WO200154477-A2.
 Homo sapiens
 02-AUG-2001.
 12-OCT-2001
 YT,
 AAM24238;
 154
 181
 214
 Query Match
 94
 121
 Local
 RESULT
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The present integrates an instruction of the present integrates an instruction of the present integrates an instruction of the properties which encodes a polypeptide with biological activity, where the polymucleotide hybridises to (I) under stringent hybridisation conditions or has greater than 99$ sequence identity with (I). (I) has respiratory, cytostatic, antiarthritic, antiaffalammatory, gastrointestinal, antiparterial, immunosuppressive, antidiabetic and antirheumatic activities, and can be used in gene therapy. (I) can be used for generating polymucleotides encoding chimeric or fusion proteins and heterologous protein sequences. The polymucleotides can be used to express recombinant protein for analysis, characterisation or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags to identify chromosomes or to map related gene positions; to compare with endogenous by sequences in patients to dentify potential genetic disorders; as probes to hybridise and discover genes, related DNA sequences; as a source of information to derive PCR
New isolated polynucleotides and polypeptides, useful for treating, e.g. cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease, Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft
 present invention describes an isolated polynucleotide (I): (a)
 Claim 20; SEQ ID NO 434; 591pp; English.
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61 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120

1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 34 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP

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93

Wang J;

Ren F, Xue A, 2A, Wang Z;

Zhang J, Ren D, Zhao QA,

Wang ω̈

requences in the process of discovering other novel polynucleotides; for sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a gene chip or other support, including for examination of expression patterns; to raise antiportion of examination of expression patterns; to raise antiportion immunication techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. The polynucleotides and polypeptides can also be used as mutritional sources or supplements, e.g. as a protein or amino acid supplement, as a carbon source, as a nitrogen source or as a source of carbohydrates. The compositions are useful for promoting better or faster closure of non-healing wounds, for the generation and resement of lung or liver fibrosis, protection or regeneration and treatment of lung or liver fibrosis, protection or regeneration and treatment of lung or liver fibrosis, protection or regeneration and treatment of lung or liver fibrosis, systemic cytokine damage. The compositions can also be used to treat inflammatory conditions (e.g. arthritis, inflammatory bowel disease or crown safet versus host disease. The present sequence represents a novel thuman polypeptide sequence from the present sequence represents a novel of the composition of the present invention. N.B. The sequence of the composition of the present invention. N.B. The sequence of the composition of the present invention. US patent US20040048249A1. 

Sequence 256 AA;

DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180 154 STTVLELSEAFTLANCSHENGTKPSYTWLKDGKPLLANDSRWLLSPDQKVLTITRVLMEDDD 213 34 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 93 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP Gaps ö Length 256; 2; Indels Score 1014; DB 8; Pred. No. 4.6e-80; 5; Mismatches 214 LDSCVVENPINQGRTLPCKITVYKKSS 240 181 LYSCMVENPISQGRSLPVKITVYRRSS 207 97.0%; Matches 200; Conservative Query Match Best Local Similarity 61 94 121 g δ g ò g à

ADM87787 standard; protein; 256 AA (first entry) 03-JUN-2004 ADM87787; 

Human EST derived amino acid sequence SEQ ID NO:880.

respiratory; cytostatic; antiarthritic; antiinflammatory; gastrointestinal; antibacterial; lamunosupressive; antidiabetic; antitheumatic; gene therapy; molecular weight marker; chromosome marker; chromosome tag; genetic fingerprinting; nutritional supplement; cancer; inflammatory condition; arthritis; inflammatory bowel disease; crohn's disease; sepsis; rhumatoid arthritis; diabetes mellitus type 1; graft versus host disease; human; expressed sequence tag; EST.

Homo sapiens

WO2004009834-A2

19-JUL-2002; 2002WO-US022858

21-JUL-2001; 2001US-0306971P. 28-MAR-2002; 2002US-00112944.

(NUVE-) NUVELO INC.

<u>ن</u> Wang À F, Xue / Wang Z; Zhang J, Ren D, Zhao QA, Weng G, 7 Yang Y, Wen , Ghosh MJ, Wehrman T, ĭ, Tang

2004-143291/14. WPI; 2004-143291/ N-PSDB; ADM87569.

New isolated polynucleotides and polypeptides, useful for treating, e.g. cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease, Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft versus host disease.

Example 2; SEQ ID NO 880; 591pp; English.

use; as markers for tissues in which the Corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags to identify chromosomes or to map related gene chromosome with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridise and discover genes, related DNA sequences; as a probe to subtract-out known sequences in the process of discovering other novel polymuclectides; for selecting and making oligomers for attachment to a gene chip or other support, including for examination of expression patterns; to raise anti-DNA antibodies or elicit another immune response. The protein antibodies and polymetides can also be used as an untritional sources or supplements, e.g. as a protein or amino acid supplement, as a carbon cource, as a nitrogen source or as a source of carbohydrates. The compositions are useful for promoting better or faster closure of non-healing wounds, for the generation and regeneration of tissues, for gut experiention injury in various tissues, and conditions resulting from systemic cytokine damage. The compositions can also be used to treat inflammatory conditions (e.g. arthritis, inflammatory bowel disease or crown state host disease or crown state or crown services.

The control of sequence or an expense or conditions resulting from systemic cytokine damage. The present conditions resulting from cytakt versus host disease. The present sequence from the present expressed sequence the derived arthritis, diabetes mellitus type 1 continued are sequence from the present expressed sequence the derived are the present expressed sequence the derived are the present cytokined. The present invention describes an isolated polynucleotide (I): (a) comprising a nucleotide sequence selected from SEQ ID NO:1-244; or (b) which encodes a polypetide with biological activity, where the polynucleotide hybridises to (I) under stringent hybridisation conditions or has greater than 99% sequence identity with (I). (I) has respiratory, cytostatic, antiarthritic, antiantlammatory, gastrointestinal, antibarthritic, antiantlammatory, antibacterial, immunosuppressive, antidiabetic and antirheumatic activities, and can be used in gene therapy. (I) can be used for activities, and can be used in gene therapy. (I) can be used for heterologous protein sequences. The polynucleotides can be used to express recombinant protein for analysis, characterisation or therapeutic use; as markers for tissues in which the corresponding protein is invention. N.B. The sequences for this patent were obtained JSPTO web site from an equivalent US patent US20040048249A1.

Sequence 256 AA;

Gaps ; 0 97.0%; Score 1014; DB 8; Length 256; 96.6%; Pred. No. 4.6e-80; ive 4; Mismatches 3; Indels ( Best Local Similarity 96.6 Matches 200; Conservative Query Match

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61 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120 153 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLGA

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121 STIVLELSEAFILNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMBDDD 180 STIVLELSEAFTLACSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 213

Search completed: July 26, 2005, 16:07:34 Job time : 59.8945 secs

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July 26, 2005, 15:58:52; Search time 15.2841 Seconds (without alignments) 1011.008 Million cell updates/sec
 1045
1 VNITSPVRLIHGTVGKSALL......NPISQGRSLPVKITVYRRSS 207
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 US-10-706-691-22
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Total number of hits satisfying chosen parameters:

513545 seqs, 74649064 residues

Searched:

Scoring table:

Perfect score:

Title:

Run on:

Sequence:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

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/cgn2\_6/ptodata/1/iaa/Re\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/PcTUS\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/PcTUS\_COMB.pep:\* Issued Patents AA: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|        |       | عن    |        |      | SUMMARIES          |                    |   |
|--------|-------|-------|--------|------|--------------------|--------------------|---|
| Result |       | Query | ;      |      | :                  |                    |   |
| 02     | Score | Match | Length | BB : | ID                 | Description        |   |
| 1      | 268   | 25.6  | 450    | 4    | US-09-907-794A-320 | Sequence 320, App  |   |
| 7      | 268   | 25.6  | 450    | 4    | US-09-905-125A-320 | 320,               |   |
| e      | 268   | 25.6  | 450    | 4    | -09                | 320,               |   |
| 4      | 268   | 25.6  | 450    | 4    | US-09-906-700-320  | 320,               |   |
| Ś      | 268   | 25.6  | 450    | 4    | US-09-903-603A-320 | 320,               |   |
| 9      | 268   | 25.6  | 450    | 4    | US-09-904-920A-320 | 320,               |   |
| 7      | 268   | 25.6  | 450    | 4    | -60                | 32                 |   |
| 60     | 268   | 25.6  | 450    | 4    |                    | 320,               |   |
| 60     | 268   | 25.6  | 450    | 4    | -60                | 35                 |   |
| 10     |       | 15.6  | 826    | 4    |                    | 16                 |   |
| 11     | 163.5 | 15.6  | 904    | 4    | US-09-877-730-6    | 9                  |   |
| 12     | 163.5 | 15.6  | 907    | 4    |                    | 20                 |   |
| 13     | 163.5 | 15.6  | 985    | 4    |                    | 10,                |   |
| 14     | 163.5 | 15.6  | 166    | 4    | US-09-877-730-12   | 12                 |   |
| 15     | 163.5 | 15.6  | 1069   | 4    | - 1                | 7                  |   |
| 16     | 163.5 | 15.6  | 1072   | 4    | US-09-877-730-18   | 18                 |   |
| 17     | 163.5 | 15.6  | 1150   | 4    | US-09-877-730-8    | 8                  |   |
| 18     | 163   | 15.6  | 316    | 4    | US-09-397-243D-13  | Sequence 13, Appl  |   |
| 19     | 161.5 | 15.5  | 300    | 4    | US-09-254-465A-10  | 10                 |   |
| 20     | 161.5 | 15.5  | 300    | 4    | US-09-397-243D-12  | 12,                |   |
| 21     | 161.5 | 15.5  | 300    | 4    | US-09-953-499-10   | 10,                | ٠ |
| 22     | 161   | 15.4  | 321    | 9    | 5169835-17         | . 516              |   |
| 23     | 191   | 15.4  | 321    | 9    | 5169835-17         | Patent No. 5169835 |   |
| 24     | 191   | 15.4  | 344    | ~    | US-08-602-725-34   | Sequence 34, Appl  |   |
| 25     | 159   | 15.2  | 248    | 9    | 5169835-15         | . 51               |   |
| 56     | 159   | 15.2  | 248    | 9    | 5169835-15         | Patent No. 5169835 |   |
| 27     | 159   | 15.2  | 365    | 4    | US-09-949-016-7591 | Sequence 7591, Ap  |   |

| 28         157.5         15.1         270         4         US-09-254-465A-24         Sequence 24, 29, 24, 24, 24, 24, 24, 24, 24, 24, 24, 24                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 24, Appl<br>26, Appl<br>26, Appl<br>22, Appl<br>22, Appl<br>6, Appli<br>6, Appli<br>23, Appl<br>23, Appl<br>23, Appl<br>23, Appl<br>23, Appl<br>23, Appl<br>24, Appl<br>25, Appl<br>25, Appl<br>26, Appl<br>27, Appl<br>27, Appl<br>28, Appl<br>28, Appl<br>29, Appl<br>331, Appl<br>311, Appl<br>311, Appl<br>311, Appl<br>311, Appl<br>311, Appl<br>311, Appl<br>311, Appl<br>311, Appl                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
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| 15.1 270 4 US-09-254-465A-24 15.1 270 4 US-09-953-499-24 15.1 273 4 US-09-953-499-24 15.1 273 4 US-09-254-465A-26 15.1 319 1 US-08-597-495B-22 15.1 319 4 US-09-064-051A-22 15.1 319 4 US-09-064-051A-22 15.0 260 4 US-09-254-465A-23 15.0 260 4 US-09-953-499-23 15.0 260 4 US-09-953-499-23 15.0 263 4 US-09-953-499-23 15.0 263 4 US-09-953-499-23 15.0 263 4 US-09-953-499-23 15.0 263 4 US-09-953-499-23 15.0 263 4 US-09-188-930-189 15.0 299 3 US-09-188-930-33 15.0 299 3 US-09-188-930-31 15.0 299 4 US-09-254-465A-1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 15.1<br>15.1<br>15.1<br>15.1<br>15.1<br>15.1<br>15.1<br>15.1<br>15.1<br>15.1<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0<br>15.0 | Sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence seq |
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# ALIGNMENTS

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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT APPLICATION NUMBER: US 60/1414
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-36
PRIOR FILING DATE: 1999-07-36
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
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PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-13
PRIOR PLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PLING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21090
Sequence 320, Application US/09907794A Patent No. 6635468
 Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
 Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
 Ferrara, Napoleone
Filvaroff, Ellen
 Hillan, Kenneth, J
 Gerber, Hanspeter
Gerritsen, Mary E.
 Kljavin, Ivar J.
Mather, Jennie P.
 GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
 Desnoyers, Luc
Eaton, Dan L.
 Fong, Sherman
Gao, Wei-Qiang
 Goddard, A.
 Pan, James
 APPLICANT:
APPLICANT:
 APPLICANT
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
 PRIOR APPLICATION NUMBER: PCIT/USOU/04414
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-26
PRIOR PLICATION NUMBER: US 60/145,698
PRIOR PLICATION NUMBER: PCT/US99/20594
PRIOR PLICATION NUMBER: PCT/US99/20594
PRIOR PLICATION NUMBER: PCT/US99/21090
PRIOR PLILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 FILING DATE: 1999-10-05
 ; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-905-125A-320
 US-09-902-775A-320
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 57 TLRPDYRDRIRLF-ENGSLLLSDLQLADEGTYEVEISIT-DDTFTGEKTINLTVDVPISR 114
 POVLV-ASTIVLELSEAFILNCSHENGIKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITR 173
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 20 LKVTVPSHTVHGVRGQALYLPVHYGFHTPASDIQII-WLFERPHTMPKYLLGSVNKSVVP 78
 1 VNITSPVRLIHGTVGKSALLSVQYS--STSSDRPVVKWQLKR--DKPVTVVQSIGTEVIG 56
 Gaps
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 Query Match 25.6%; Score 268; DB 4; Length 450; Best Local Similarity 31.9%; Pred. No. 2.2e-18; Matches 67; Conservative 43; Mismatches 90; Indels
 197 VTKEDIGNYSCLVRNPVSEMESDIIMPIIY 226
 174 VLMEDDDLYSCMVENPISQGRSLPVKITVY 203
FRIOR FILING DATE: 1999-015

PRIOR PELICATION NUMBER: PCT/US99/21089

PRIOR FILING DATE: 1999-10-05

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PRIOR PILING DATE: 1999-11-29

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PRIOR FILING DATE: 1999-12-02

PRIOR PILING DATE: 1999-12-02

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PRIOR PILING DATE: 1999-12-06

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PRIOR PILING DATE: 1999-12-16

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PRIOR PILING DATE: 1999-12-20

PRIOR PILING DATE: 1999-12-20

PRIOR PILING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423

SEQ ID NO 320
 US-09-905-125A-320
; Sequence 320, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
 Godowski, Paul J.
Grimaldi, Christopher J.
 Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Cjang
Gerber, Hanspeter
Gerittsen, Mary E.
 Gurney, Austin L.
Hillan, Kenneth, J
 Pan, James
Paoni, Nicholas F.
 Roy, Margaret Ann
 Kljavin, Ivar J.
Mather, Jennie P.
 APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
 Desnoyers, Luc
Eaton, Dan L.
 Goddard, A.
 ORGANISM: Homo Sapien
 US-09-907-794A-320
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57 TLRPDYRDRIRLF-ENGSLLLSDLQLADEGTYEVEISIT-DDTFTGEKTINLTVDVPISR 114
 115 PQVLV-ASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITR 173
 1 VNITSPVRLIHGTVGKSALLSVQYS--STSSDRPVVKWQLKR--DKPVTVVQSIGTEVIG 56
 20 LKVTVPSHTVHGVRGQALYLPVHYGFHTPASDIQII-WLFERPHTWPKYLLGSVNKSVVP 78
 25.6%; Score 268; DB 4; Length 450; 31.9%; Pred. No. 2.2e-18;
 Indels
 Query Match 25.6%; Score 268; DB Best Local Similarity 31.9%; Pred. No. 2.2e-Matches 67; Conservative 43; Mismatches
 197 VTKEDIGNYSCLVRNPVSEMESDIIMPIIY 226
 174 VLMEDDDLYSCMVENPISOGRSLPVKITVY 203
 PRIOR FILING DATE: 1999-10-05
PRIOR PELICATION WUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR PELICATION WUMBER: PCT/US99/28313
PRIOR PLING DATE: 1999-11-30
PRIOR PLING DATE: 1999-11-30
PRIOR PELICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR PELICATION NUMBER: PCT/US99/30095
PRIOR PELICATION NUMBER: PCT/US99/30095
PRIOR PELICATION NUMBER: PCT/US99/30091
PRIOR PELICATION NUMBER: PCT/US99/30910
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PRIOR PELICATION NUMBER: PCT/US99/3099
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PRIOR PELING DATE: 1999-12-20
PRIOR PELING DATE: 1999-12-20
PRIOR PELING DATE: 1099-12-20
PRIOR PELING DATE: 1099-12-20
PRIOR PELICATION NUMBER: PCT/US00/00219
PRIOR PELING DATE: 2000-01-05
PRIOR PELING DATE: 2000-01-05
 FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
PILING DATE: 1999-07-28
APPLICATION NUMBER: PCT/US99/20594
FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
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 ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITLE OF INVENTION: Acids Encoding the Same
 TITLE OF INVENTION: ACIDE ENCOUTING LIE SORIES
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT PILIG DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/145,048
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
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Sequence 320, Application US/09902775A
 Godowski, Paul J.
Grimaldi, Christopher J.
 Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Olang
Gerber, Hanspeter
 Williams, P. Mickey Wood, William, I.
 Timothy A.
 Gurney, Austin L.
Hillan, Kenneth, J.
 Gerritsen, Mary E
 Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
 Paoni, Nicholas F.
 Roy, Margaret Ann
Stewart, Timothy I
Tumas, Daniel
 Genentech, Inc.
Ashkenazi, Avi
Botstein, David
 Desnoyers, Luc
Eaton, Dan L.
 TYPE: PRT
CRGANISM: Homo Sapien
US-09-902-775A-320
 Goddard,
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57 TLRPDYRDRIRLF-ENGSLLLSDLQLADEGTYEVEISIT-DDTFTGEKTINLTVDVPISR 114
 115 PQVLV-ASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITR 173
 20 LKVTVPSHTVHGVRGQALYLPVHYGFHTPASDIQII-WLFERPHTMPKYLLGSVNKSVVP
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14.

FILE REFERENCE: 10466-14.

CURRENT APPLICATION NUMBER: US/09/906,700

CURRENT FILING DATE: 2000-09-18

PRIOR PAPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 1090-07-07

PRIOR PLICATION NUMBER: US 60/143,048

PRIOR PAPLICATION NUMBER: US 60/145,698

PRIOR PLING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-26
 1 VNITSPVRLIHGTVGKSALLSVQYS--STSSDRPVVKWQLKR--DKPVTVVQSIGTEVIG
 10;
25.6%; Score 26%; DB 4; Length 450; 31.9%; Pred. No. 2.2e-18; tive 43; Mismatches 90; Indels
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PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
 FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
 APPLICATION NUMBER: PCT/US99/21090
 PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
 Sequence 320, Application US/09906700 Patent No. 6723535
 Godowski, Paul J.
Grimaldi, Christopher J.
 Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
 Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
 Ferrara, Napoleone
Filvaroff, Ellen
 Hillan, Kenneth, J
 Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
 Gerritsen, Mary E
 Pan, James
Paoni, Nicholas F
 1999-09-13
 Gurney, Austin L.
 Mather, Jennie P.
Query Match
Best Local Similarity 31.9%
Matches 67; Conservative
 Kljavin, Ivar J
 APPLICANT: Genentech, Inc..
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
 -09-906-700-320
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AFPLICANT:

ATTILE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
CURRENT APPLICATION NUMBER: US/09/903,603A
CURRENT PILING DATE: 2001-07-11
PRIOR PILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PAPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-03
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
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 1 VNITSPVRLIHGTVGKSALLSVQYS--STSSDRPVVKWQLKR--DKPVTVVQSIGTEVIG 56
 20 LKVTVPSHTVHGVRGQALYLPVHYGFHTPASDIQII-WLFERPHTWFKYLLGSVNKSVVP 78
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25.6%; Score 260; DB 4; Length 450;
L Similarity 31.9%; Pred. No. 2.2e-18;
67; Conservative 43; Mismatches 90; Indels
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 174 VLMEDDDLYSCMVENPISQGRSLPVKITVY 203
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PRIOR FILING DATE: 1999-10-05
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PRIOR FILING DATE: 1999-11-29
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PRIOR PILING DATE: 1999-11-30
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PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 320
 FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
FIPLING DATE: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
 Williams, P. Mickey Wood, William, I.
 TYPE: PRT
ORGANISM: Homo Sapien
 Query Match
Best Local Similarity
Matches 67; Conserv
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 79 DL--EYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGTLSASQKIQVTVDDPVTK 136
 57 TLRPDYRDRIRLF-ENGSLLLSDLQLADEGTYEVEISIT-DDTFTGEKTINLTVDVPISR 114
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PRIOR APPLICATION NUMBER: PCT/US99/23089
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PRIOR FILING DATE: 1999-12-02
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 Sequence 320, Application US/09903603A
Patent No. 6767995
GENERAL INFORMATION:
 Godowski, Paul J.
Grimaldi, Christopher J.
 Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
 Gurney, Austin L.
Hillan, Kenneth, J.
 Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
 Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
 Kljavin, Ivar J.
Mather, Jennie P.
 Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
 1 Similarity
67; Conserva
 Рап, Јашев
 Homo Sapien
 -09-903-603A-320
 ; TYPE: PRT
; ORGANISM: Hom
US-09-906-700-320
 Query Match
Best Local S:
Matches 67
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 APPLICANT:
APPLICANT:
APPLICANT:
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115 POVLV-ASTTVLELSEAFTINCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITR 173 RESULT 6 US-09-904-920A-320 ; Sequence 320, Application US/09904920A

Gaps

Gaps

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 20 LKVTVPSHTVHGVRGQALYLPVHYGFHTPASDIQII-WLFERPHTMPKYLLGSVNKSVVP 78
 1 VNITSPVRLIHGTVGKSALLSVQYS--STSSDRPVVKWQLKR--DKPVTVVQSIGTEVIG
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIILE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
 10;
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 Indels
 90,
; Score 268; DB 4;
; Pred. No. 2.2e-18;
43; Mismatches 90;
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PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
 FILING DATE: 1999-07-28
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 FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
 PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
 Sequence 320, Application US/09909064
Patent No. 6818449
 Godowski, Paul J.
Grimaldi, Christopher
 Williams, P. Mickey Wood, William, I.
 Query Match
Best Local Similarity 31.9%;
Matches 67; Conservative 43
 Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
 Ferrara, Napoleone
Filvaroff, Ellen
 Hillan, Kenneth, J
 Gerber, Hanspeter
Gerritsen, Mary E
 1999-09-08
 FILING DATE: 1999-09-15
 999-09-13
 Gurney, Austin L.
 Kljavin, Ivar J.
Mather, Jennie P.
 Botstein, David
 Wei-Qiang
 Ashkenazi, Avi
 APPLICANT: Genentech, Inc.
 Eaton, Dan L.
 Tumas, Daniel
 Goddard, A.
 Pan, James
 FILING DATE:
 FILING DATE:
 JS-09-909-064-320
 APPLICANT:
APPLICANT:
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 CURRENT PILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/USOO/04414
PRIOR FILING DATE: 2000-02-22
PRIOR PELICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
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 FILE REPERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,920A
CURRENT FILING DATE: 2001-07-13
 Godowski, Paul J.
Grimaldi, Christopher J.
 Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
 Williams, P. Mickey Wood, William, I.
 Ferrara, Napoleone
Filvaroff, Ellen
 Timothy A.
 Pan, James
Paoni, Nicholas F.
 Gerber, Hanspeter
Gerritsen, Mary E
 Roy, Margaret Ann
 Desnoyers, Luc
Eaton, Dan L.
 Wei-Qiang
 Fong, Sherman
 Tumas, Daniel
 Goddard, A.
 TYPE: PRT
ORGANISM: Homo Sapien
US-09-904-920A-320
 Stewart,
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and Transmembrane Polypeptides and Nucleic
 APPLICANT: WILLIABMU, F. MILCASY
APPLICANT: WOOD, WILLIABMU, F. MILCANT
TITLE OF INVENTION: Secreted and Transmembrane F. TITLE OF INVENTION: Secreted and Transmembrane F. TITLE OF INVENTION: Secreted and Transmembrane F. TITLE OF INVENTION: Acids Encoding the Same FILES REPERBENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,381A
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PRIOR PILING DATE: 1999-07-07
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 ORGANISM: Homo Sapien
US-09-905-381A-320
 TYPE: PRT
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 57 TLRPDYRDRIRLF-ENGSLILSDLQLADEGTYEVEISIT-DDTFTGEKTINLTVDVPISR 114
 PQVLV-ASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITR 173
 20 LKVTVPSHTVHGVRGQALYLPVHYGFHTPASDIQII-WLFERPHTMPKYLLGSVNKSVVP 78
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 174 VLMEDDDLYSCMVENPISQGRSLPVKITVY 203
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PLILING DATE: 1999-11-29
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PRIOR FLILING DATE: 1999-12-0
PRIOR FLILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
 Sequence 320, Application US/09905381A
Patent No. 6818746
GENERAL INFORMATION:
 Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
 Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Clang
Gerber, Hanapeter
Gerritsen, Mary E.
 Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
 Pan, James
Paoni, Nicholas F.
 Kljavin, Ivar J.
Mather, Jennie P.
 APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
 Desnoyers, Luc
Eaton, Dan L.
 Goddard, A.
 TYPE: PRT
ORGANISM: Homo Sapien
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 57 TLRPDYRDRIRLF-ENGSLILLSDLQLADEGTYEVEISIT-DDTFTGEKTINLTVDVPISR 114
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 US-09-906-618-320
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; Patent No. 6828146
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Gaps

10;

Indels

Mismatches

43;

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Best Local Similarity 31.9%
Matches 67; Conservative
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 PPLICANT: Thmas, Daniel
PPLICANT: Williams, P. Mickey
PPLICANT: Wood, William, I.
ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
 CURRENT AFFILMS NUMBER: 05,001-07-16
PRIOR APPLICATION NUMBER: PCT/USGO/04414
PRIOR PILING DATE: 2000-02-22
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PRIOR PILING DATE:
 FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,618
 Godowski, Paul J.
Grimaldi, Christopher J.
 Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
 Roy, Margaret Ann
Stewart, Timothy A.
 Ferrara, Napoleone
Filvaroff, Ellen
 Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
 Pan, James
Paoni, Nicholas F.
 Fong, Sherman
 Goddard, A.
 TYPE: PRT
ORGANISM: Homo Sapien
 US-09-906-618-320
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DB 4; Length 450;

25.6%; Score 268;

Query Match

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APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Sambrowicz, Brian
APPLICANT: Sambrowicz, Brian
APPLICANT: Sambrowicz, Brian
APPLICANT: Samds, Arthur T.
TILE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the FILE REFERENCE: LEX.-0189-USA
CURRENT APPLICATION NUMBER: US/09/877,730
CURRENT APPLICATION NUMBER: US 60/210,607
PRIOR PILING DATE: 2000-06-09
NUMBER OF SEC ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SEC ID NO 16
LENGTH: 826
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 62 YRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVAS 121
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 168 VLTITRVLMEDDDLYSCMVENPISQGRSLP-VKITV 202
 | | ::: ||| :| || || || || 302 -LVINQIIPEDDAIYQCMAEN--SQGSILSRARLTV 334
 197 VTKEDIGNYSCLVRNPVSEMESDIIMPIIX 226
 174 VLMEDDDLYSCMVENPISQGRSLPVKITVY 203
 Sequence 16, Application US/09877730 Patent No. 6465632
 Sequence 6, Application US/09877730 Patent No. 646563. GENERAL INFORMATION: APPLICANT: Walke, D. Wade
 ORGANISM: homo sapiens
US-09-877-730-16
 -09-877-730-16
 JS-09-877-730-6
 TYPE: PRT
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APPLICANT: Scoville, John
APPLICANT: Scoville, John
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Tambrowicz, Brian
APPLICANT: Sambrowicz, Brian
APPLICANT: Sambrowicz, Brian
APPLICANT: Sambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the
TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the
CURRENT APPLICATION NUMBER: US/09/877,730
CURRENT APPLICATION NUMBER: US/09/877,730
CURRENT PILLING DATE: 2001-06-09
NUMBER OF SEQ ID NOS: 31
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 62 YRDRIRLFENGSLILLSDLOLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVAS 121
 122 TTVL-----ELSEAFT-----LNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQK 167
 165 NITTS---LHQTV-----VLECMATGNPKPIISWSRLDHKSIDV---FNTRVLG---- 207
 62 YRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVAS 121
 122 TTVL-----ELSEAFT-----LNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQK 167
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 168 VLTITRVLMEDDDLYSCMVENPISOGRSLP-VKITV 202
 302 -LVINQIIPEDDAIYQCMAEN--SQGSILSRARLTV 334
 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10 LENGTH: 985
 Sequence 12, Application US/09877730; Patent No. 6465632; GENBRAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Scoville, John
APPLICANT: Friedrich, Glenn
APPLICANT: Friedrich, Glenn
APPLICANT: Abuin, Alejandro
APPLICANT: Zambrowicz, Brian
 Sequence 10, Application US/09877730 Patent No. 6465632
 ; TYPE: PRT
; ORGANISM: homo sapiens
US-09-877-730-10
 GENERAL INFORMATION:
 RESULT 14
US-09-877-730-12
 -09-877-730-10
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 DEFINITION TO WARDEN TO WA
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: NO. 6465632el Human Phosphatases and Polynucleotides Encoding the FILE REFERENCE: LEX-0189-USA
CURRENT FILING DATE: 2001-06-08
RIOR APPLICATION NUMBER: US 60/210,607
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 904
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 62 YRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVAS 121
 122 TTVL----ELSEAFT----LNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQK 167
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Matches 58; Conservative 34; Mismatches 63; Indels 61;
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 380 -LVINQIIPEDDAIYQCMAEN--SQGSILSRARLTV 412
 168 VLTITRVLMEDDDLYSCMVENPISQGRSLP-VKITV 202
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 Sequence 20, Application US/09877730 Patent No. 6465632
 TYPE: PRT
ORGANISM: homo sapiens
US-09-877-730-6
 ORGANISM: homo sapiens
 GENERAL INFORMATION:
 US-09-877-730-20
 US-09-877-730-20
 SEQ ID NO 20
LENGTH: 907
 TYPE: PRT
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Search completed: July 26, 2005, 16:15:54 Job time : 16.2841 secs
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APPLICANT: Sands, Arthur T.

TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the FILE REFERENCE: LEX-0189-038 CURRENT APPLICATION NUMBER: US/09/877,730 CURRENT APPLICATION NUMBER: US 60/210,607 PRIOR PRILAG APPLICATION NUMBER: US 60/210,607 PRIOR FILING DATE: 2000-06-09 NUMBER OF SEQ ID NOS: 31 06-09 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12 LENGTH: 991
 APPLICANT: Sands, Arthur T.

TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the FILE REFERENCE: LEX.0189-USA
CURRENT APPLICATION NUMBER: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,607
PRIOR PILING DATE: 2000-06-09
PRIOR PILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
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 243 NITTS---LHQTV------VLECMATGNPKPIISWSRLDHKSIDV---FNTRVLG---- 285
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 DB 4; Length 1069;
 Length 991;
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 302 -LVINQIIPEDDAIYOCMAEN--SOGSILSRARLTV 334
 168 VLTITRVLMEDDDLYSCMVENPISOGRSLP-VKITV 202
 Query Match
15.6%; Score 163.5; DB 4;
Best Local Similarity 26.9%; Pred. No. 2.1e-07;
Matches 58; Conservative 34; Mismatches 63;
 APPLICANT: Walke, D. Wade
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
 Sequence 2, Application US/09877730 Patent No. 6465632
 Abuin, Alejandro
Zambrowicz, Brian
 ; TYPE: PRT
; ORGANISM: homo sapiens
US-09-877-730-12
 ; TYPE: PRT
; ORGANISM: homo sapiens
US-09-877-730-2
 LENGTH: 1069
 RESULT 15
US-09-877-730-2
 APPLICANT:
APPLICANT:
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--LNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQK 167
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 GEMERAL INFORMATION:

APPLICANT: Davids, Andrew Robert
APPLICANT: Pagan, Richard Joseph
APPLICANT: Pedan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Power, Christine
APPLICANT: Power, Christine
APPLICANT: Boschert, Ursula
ITILE OF INVENTION: Cytokine antagonist molecules
FILE REFERENCE: 674582-2001
CURRENT APPLICATION NUMBER: US/10/706,691
CURRENT PILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: GB 0209884.6
PRIOR APPLICATION NUMBER: GB 0209884.6
PRIOR RILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: GB 0209884.6
NUMBER OF SEQ ID NOS: 43
SOFTWARE: SeqWin99, version 1.02
LENGTH: 207
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 ALIGNMENTS
 Sequence 22, Application US/10706691; Publication No. US20040204352A1; GENERAL INFORMATION:
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US-10-706-691-22
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880, App
24, Appl
 (without alignments)
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Sequence 880,
Sequence 24, A
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Sequence 26, A
Sequence 16, A
Sequence 116, A
 Description
 US-10-706-691-22
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1 VNITSPVRLIHGTVGKSALL......NPISQGRSLPVKITVYRRSS
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 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 US-10-706-691-22
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US-10-10-944-434
US-10-112-944-880
 Total number of hits satisfying chosen parameters:
 1741741 segs, 388992284 residues
 SUMMARIES
 Applications AA:
 Listing first 45 summaries
 - protein search, using sw model
 Gapop 10.0 , Gapext 0.5
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 Post-processing: Minimum Match 0%
Maximum Match 100%
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 Length
 Published
 BLOSUM62
 Query
 100.0
100.0
100.0
100.0
98.5
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Gaps

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Result

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; TITLE OF INVENTION: Cytokine antagonist molecules; FILE REFERENCE: 674582-2001; CURRENT APPLICATION NUMBER: US/10/706,691; CURRENT APPLICATION NUMBER: US/10/706,691; CURRENT FILING DATE: 2003-04-30; PRIOR APPLICATION NUMBER: PCT/GB03/01851; PRIOR FILING DATE: 2003-04-30; PRIOR FILING DATE: 2002-04-30; NUMBER OF SEQ ID NOS: 43; SOFTWARE: SeqWin99, version 1.02; SEQ ID NO 43; TENGTH: 246; TYPE: PRT: TYPE: T
 Sequence 4, Application US/10432103; Publication No. US20040043424A1; ENDICATION: APPLICANT: INCYTE GENOMICS, INC. APPLICANT: BAUGHN, Mariah R.; APPLICANT: LU, Dyung Aina M. APPLICANT: YUE, Henry
 US-10-432-103-4
 -10-432-103-4
 Query Match
 8
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 61 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 61 DYRDRIRLFENGSLILSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 94 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 153
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Best Local Similarity 100.0%; Pred. No. 6.1e-88;
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Sequence 20, Application US/10706691
Sequence 20, Application US/10706691
Sequence 20, Application US/10706691
Sequence 20, Sequenc
 Sequence 43, Application US/10706691
Publication No. US20040204352A1
GENERAL INFORMATION:
APPLICANT: Davids, Andrew Robert
APPLICANT: Pagan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin;
APPLICANT: Power, Christine
APPLICANT: Chvatchko, Yolande
APPLICANT: Boschert, Ursula
 181 LYSCMVENPISQGRSLPVKITVYRRSS 207
 LYSCMVENPISQGRSLPVKITVYRRSS 207
 214 LYSCMVENPISQGRSLPVKITVYRRSS 240
 181 LYSCMVENPISQGRSLPVKITVYRRSS 207
 TYPE: PRT
ORGANISM: Homo sapiens
 US-10-706-691-43
 US-10-706-691-20
 SEQ ID NO 20
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 181
 121
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8

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 94 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 153
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Query Match
Best Local Similarity 100.0%; Pred. No. 6.3e-88;
Matches 207; Conservative 0; Mismatches 0; Indels 0;
 Length 298;
 LCKi S.

AVELU, Kavitha

RAMKGWAR, Jayalaxmi

LU, Yan

LU, Yan

LU, Yan

LU, Yan

APPLICANT: GUNDHI, Ramena R.

APPLICANT: GRADHI, Ameena R.

APPLICANT: GANDHI, Ameena R.

APPLICANT: APOMONIQUE G.

TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS

FILE REFERENCE: PF-0441 PCT

CURRENT APPLICATION NUMBER: 60/249,645

PRIOR APPLICATION NUMBER: 60/249,645

PRIOR PLILING DATE: 2000-11-16

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PERL PROGRAM

SEQ ID NOS: 12

LENGTH: 298

TYPE: PRT

ORCF.
 NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20040043424A1 5831801CD1
 DB 15;
 100.0%; Score 1045;
 181 LYSCMVENPISOGRSLPVKITVYRRSS 207
 214 LYSCMVENPISQGRSLPVKITVYRRS 240
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 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 94 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 153
 STIVLELSEAFTLNCSHENGTKPSYTWLKDGKPLINDSRMLLSPDQKVLTITRVLMEDDD 180
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 61 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 34 VNITSPVRLIHGITUGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 93
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 60
 1 VNITSPVRLIHGIVGKSALLSVQXSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 60
 0; Gaps
 0; Gaps
 Query Match 100.0%; Score 1045; DB 16; Length 383; Best Local Similarity 100.0%; Pred. No. 1.1e-87; Matches 207; Conservative 0; Mismatches 0; Indels 0;
. 8.1e-88;
-hes 0; Indels
 Sequence 26, Application US/10706691

Sequence 26, Application US/10706691

GENERAL INFORMATION:
APPLICANT: Davids, Andrew Robert
APPLICANT: Fagan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Christine
APPLICANT: Christine
APPLICANT: Christine
TITLE OF INVENTION: Cytokine antagonist molecules
TITLE OF INVENTION: Cytokine antagonist molecules
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: US/10/706,691
CURRENT FILING DATE: 2003-04-30
PRIOR APPLICATION NUMBER: PCT/GB03/01851
PRIOR PILING DATE: 2002-04-30
NUMBER: OF SEQ ID NOS: 43

NUMBER: SEQ ID NOS: 43

SEQ ID NO SE SEQ ID NOS: 43

LENDTH: 383
 100.0%; Preq. .v..
 214 LYSCMVENPISQGRSLPVKITVYRRSS 240
 181 LYSCMVENPISQGRSLPVKITVYRRSS 207
 LYSCMVENPISOGRSLPVKITVYRRSS 207
 LYSCMVENPISQGRSLPVKITVYRRSS 207
 US-10-706-691-16; Sequence 16, Application US/10706691; Sequence 16, Application US/10706691; Publication No. US20040204352A1; GENERAL INFORMATION:
 Best Local Similarity 100. Matches 207; Conservative
 ORGANISM: Homo sapiens
US-10-706-691-26
 61
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61 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 94 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 153
 121 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 154 STTVLELSEAPTINCSHENGTKPSYTWLKDGKPLINDSRWLLSPDQKVLTITRVLMEDDD 213
 93
 34 VNITSPVRLIHGITVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 Gaps
 ;
0
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 Score 1045; DB 16; Length 416;
Pred. No. 1.3e-87;
 Query Match 100.0%; Score 1045; DB 16; Length 416; Best Local Similarity 100.0%; Pred. No. 1.3e-87; Matches 207; Conservative 0; Mismatches 0; Indels 0;
 0; Indels
APPLICANT: Bavids, Andrew Robert
APPLICANT: Fagan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Power, Christine
APPLICANT: Power, Christine
APPLICANT: Charachek, Yolande
APPLICANT: Boschert, Urgula
ITTLE OF INVENTION: Cytckine antagonist molecules
FILE REFERENCE: 674582-2001
CURRENT APPLICATION NUMBER: US/10/706,691
CURRENT APPLICATION NUMBER: PCT/GB03/01851
PRIOR APPLICATION NUMBER: CT/GB03/01851
PRIOR PLING DATE: 2003-04-30
PRIOR PLING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 43
SOFTWARE: SeqWin99, version 1.02
 Sequence 41, Application US/10706691

Publication No. US20040204352A1

GENERAL INFORMATION:

APPLICANT: Davids, Andrew Robert

APPLICANT: Davids, Andrew Robert

APPLICANT: Phelps, Christopher Benjamin

APPLICANT: Phelps, Christopher Benjamin

APPLICANT: Chvatchko, Yolande

APPLICANT: Boschert, Ursula

TITLE OF INVENTION: Cytokine antagonist molecules

TITLE OF INVENTION: Cytokine antagonist molecules

FILE REFERENCE: 674582-2001

CURRENT APPLICATION NUMBER: US/10/706,691

CURRENT APPLICATION NUMBER: ECT/GB03/01851

PRIOR FILING DATE: 2003-04-30

PRIOR APPLICATION NUMBER: GB 0209884.6

PRIOR APPLICATION NUMBER: GB 0209884.6

PRIOR SEQ ID NOS: 43

SOFTWARE: SeqWin99, version 1.02

SEQ ID NO 41

TYPE: PRT
 0; Mismatches
 214 LYSCMVENPISOGRSLPVKITVYRRSS 240
 181 LYSCMVENPISOGRSLPVKITVYRRSS 207
 Query Match

Best Local Similarity 100.0%;

Matches 207; Conservative 0;
 ; ORGANISM: Homo sapiens
US-10-706-691-16
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APPLICANT:
APPLICANT:
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 154 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 213
 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 STTVLELSEAFTINCSHENGTKPSYTWLKDGKPLINDSRWLLSPDQKVLTITRVLMEDDD 213
 61 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 94 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 153
 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 94 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEXTINLTVDVFISRPQVLVA 153
 34 VNITSPVRLIHGTVGKSALLSVQYSSTSSDKPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 93
34 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 93
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 Query Match 98.5%; Score 1029; DB 16; Length 418; Best Local Similarity 98.6%; Pred. No. 3.8e-86; Matches 204; Conservative 2; Mismatches 1; Indels 0
 Sequence 18, Application US/10706691

Sequence 18, Application US/10706691

Bublication No. 200040204352A1

GENERAL INFORMATION:

APPLICANT: Pasids, Andrew Robert

APPLICANT: Phelps, Christopher Benjamin

APPLICANT: Power, Christopher Benjamin

APPLICANT: Power, Christopher Benjamin

APPLICANT: Power, Christine

APPLICANT: Power, Christine

APPLICANT: Coverche, Volande

APPLICANT: Chvatche, Volande

APPLICANT: Coverche antagonist molecules

FILE OF INVENTION: Cytckine antagonist

CURRENT APPLICATION NUMBER: US/10/706,691

CURRENT FILING DATE: 2003-11-12

PRIOR FILING DATE: 2003-04-30

PRIOR FILING DATE: 2002-04-30

NUMBER OF SEQ ID NOS: 43

SOFTWARE: SeqWin99, version 1.02

LENGTH . L
 214 LYSCVVENPISQVRSLPVKITVYRRSS 240
 214 LYSCMVENPISQGRSLPVKITVYRRSS 240
 LYSCMVENPISOGRSLPVKITVYRRSS 207
 181 LYSCMVENPISQGRSLPVKITVYRRSS 207
 TYPE: PRT
ORGANISM: Homo sapiens
US-10-706-691-18
 121
 181
 61
 154
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US-10-112-944-434
Sequence 434, Application US/10112944
Publication No. US20040048249A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Yang, Yonghong

```
61 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 94 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 153
 121 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 154 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 213
 93
 34 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 Gaps
 .
0
 APPLICANT: Ghosh, Malabika
APPLICANT: Ghosh, Malabika
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Dinwui
APPLICANT: Wang, Dinwui
APPLICANT: Wang, Dinwui
TITLE OF INVENTION: No. US20040048249Alel Nucleic Acids and
TITLE OF INVENTION: Secreted Polypeptides
TITLE OF INVENTION: Secreted Polypeptides
TITLE OF INVENTION: Secreted Polypeptides
CURRENT FILING DATE: 2000-01-21
PRIOR PEPLICATION NUMBER: US 09/491,404
PRIOR PELLING DATE: 2000-01-25
PRIOR PELLING DATE: 2000-01-25
PRIOR PELLING DATE: 2000-02-03
PRIOR PELLING DATE: 2000-02-03
PRIOR PELLING DATE: 2000-02-03
PRIOR PELLING DATE: 2000-03-07
PRIOR PELLING DATE: 2000-03-19
PRIOR PELLING DATE: 2000-03-19
PRIOR PELLING DATE: 2000-03-19
PRIOR PELLING DATE: 2000-03-19
PRIOR PELLING DATE: 2000-03-19
PRIOR PELLING DATE: 2000-04-18
PRIOR PELLING DATE: 2000-04-18
PRIOR PELLING DATE: 2000-04-18
PRIOR PELLING DATE: 2000-05-18
PRIOR PELNG DATE: 2000-05-18
PRIOR PELNG DATE: 2000-05-18
 Length 256;
 Indels
 Query Match 97.0%; Score 1014; DB 15; Best Local Similarity 96.6%; Pred. No. 4.7e-85; Matches 200; Conservative 5; Mismatches 2;
 | ||:|||||:|||:|| ||||:||
LDSCVVENPINQGRTLPCKITVYKKSS 240
 181 LYSCMVENPISQGRSLPVKITVYRRSS 207
 ; Sequence 880, Application US/10112944; Publication No. US20040048249A1; GENERAL INFORMATION:
Weng, Gezhi
Zhang, Jie
Ren, Feiyan
Xue, Aidong J.
Wang, Jian-Rui
Wehrman, Tom
Ghosh, Malabika
 APPLICANT: Tang, Y. Tom
APPLICANT: Yang, Yonghong
APPLICANT: Weng, Gezhi
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Xue, Aldong J.
APPLICANT: Weng, Jian-Rui
APPLICANT: Wehrman, Tom
 ORGANISM: Homo sapiens
 RESULT 10
US-10-112-944-880
 US-10-112-944-434
```

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Sequence 4, Application US/10706691
Publication No. US20040204352A1
GENERAL INFORMATION:
 Sequence 6, Application US/10706691
Publication No. US20040204352A1
GENERAL INFORMATION:
 NUMBER OF SEQ ID NOS: 43
SCFTWARE: SeqWin99, version 1.02
SEQ ID NO 24
LENGTH: 110
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-691-24
 TYPE: PRT
ORGANISM: Homo sapiens
 RESULT 13
US-10-706-691-6
 US-10-706-691-4
 SEQ ID NO 4
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 В
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 94 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLGA 153
 STIVLELSEAFILNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 154 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRWLLSPDQKVLTITRVLMEDDD 213
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 60
 34 VNITSPVRLIHGITVGKKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 93
 Gaps
 ö
 APPLICANT: Shao, Ouncat.
APPLICANT: Wang, Zhiwei
TITLE OF INVENTION: No. US20040048249Alel Nucleic Acids and
TITLE OF INVENTION: No. US20040048249Alel Nucleic Acids and
TITLE OF INVENTION: Secreted Polypeptides
FILE REFERENCE: 805A
CURRENT APPLICATION NUMBER: US/10/112,944
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR APPLICATION NUMBER: US 09/491,705
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR PILING DATE: 2000-02-28
PRIOR PELING DATE: 2000-03-07
PRIOR PLING DATE: 2000-03-07
PRIOR PLING DATE: 2000-04-04
PRIOR PILING DATE: 2000-04-18
PRIOR PILING DATE: 2000-04-18
PRIOR PILING DATE: 2000-04-18
PRIOR PILING DATE: 2000-04-18
PRIOR PILING DATE: 2000-04-18
PRIOR PILING DATE: 2000-05-18
PRIOR PILING DATE: 2000-05-18
 Length 256;
 3; Indels
 APPLICANT: Davids, Andrew Robert
APPLICANT: Fagan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Power, Christine
APPLICANT: Chvatchko, Yolande
APPLICANT: Chvatchko, Yolande
APPLICANT: Boschert, Ursula
TITLE OF INVERTION: Cytokine antagonist molecules
FILE REFERENCE: 674582-2001
CURRENT APPLICATION NUMBER: US/10/706,691
 97.0%; Score 1014; DB 15;
96.6%; Pred. No. 4.7e-85;
live 4; Mismatches 3;
 214 LYSCVVENPINQGRTLPCKITEYRKSS 240
 LYSCMVENPISQGRSLPVKITVYRRSS 207
 CURRENT FILLING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/GB03/01851
PRIOR FILLING DATE: 2003-04-30
PRIOR APPLICATION NUMBER: GB 0209884.6
PRIOR FILING DATE: 2002-04-30
 Sequence 24, Application US/10706691
Publication No. US20040204352A1
GENERAL INFORMATION:
 NUMBER OF SEQ ID NOS: 924
SOFTWARE: pt_FL_genes Version 5.0
Ghosh, Malabika
 Best Local Similarity 96.6
Matches 200; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
 US-10-112-944-880
 US-10-706-691-24
 61
 121
 181
 Query Match
 APPLICANT:
APPLICANT:
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9
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 5 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 64
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 Gaps
 Gaps
 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDV 110
 61 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDV 110
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0
 61 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDV 110
 65 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDV 114
 Length 110;
 Length 114;
 0; Indels
 Indels
 APPLICANT: Davids, Andrew Robert
APPLICANT: Fagan, Richard Joseph
APPLICANT: Fagan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Power, Christine
APPLICANT: Boschert, Ursula
TITLE OF INVENTION: CYCLOkine antagonist molecules
TITLE OF INVENTION: CYCLOkine antagonist molecules
FILE REPERBUCE: 674582-2001
CURRENT APPLICATION NUMBER: US/10/706,691
CURRENT FILING DATE: 2003-04-30
PRIOR PLING DATE: 2003-04-30
PRIOR APPLICATION NUMBER: GB 0209884.6
PRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 43
SOFTWARE: SeqWin99, version 1.02
Query Match 52.4%; Score 548; DB 16; Best Local Similarity 100.0%; Pred. No. 1.3e-42; Matches 110; Conservative 0; Mismatches 0;
 Query Match 52.4%; Score 548; DB 16; Best Local Similarity 100.0%; Pred. No. 1.4e-42; Matches 110; Conservative 0; Mismatches 0;
 APPLICANT: Davids, Andrew Robert
APPLICANT: Fagan, Richard Joseph
APPLICANT: Phelps, Christopher Benjamin
APPLICANT: Power, Christine
APPLICANT: Chvatcho, Yolande
APPLICANT: Boschert, Ursula
TITLE OF INVENTION: Cytokine antagonist molecules
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APPLICANT:
APPLICANT:
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 111 PISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLT 170
 1 PISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLT 60
 IIILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIILE OF INVENTION: Acids Encoding the Same
 Gaps
 Length 94;
 0; Indels
 46.3%; Score 484; DB 16;
100.0%; Pred. No. 8.3e-37;
iive 0; Mismatches 0;
 171 ITRVLMEDDDLYSCMVENPISQGRSLPVKITVYR 204
 61 ITRVLMEDDDLYSCMVENPISQGRSLPVKITVYR 94
FILE REFERENCE: 674582-2001
CURRENT APPLICATION NUMBER: US/10/706,691
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/GB03/01851
PRIOR FILING DATE: 2003-04-30
PRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 43
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 6
 PRIOR APPLICATION NUMBER: US 60/143,048
RRIOR FILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR FLING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PLING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
 FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,320
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
 Sequence 320, Application US/09909320 Patent No. US20020132240A1
 Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
 Williams, P. Mickey Wood, William, I.
 Roy, Margaret Ann
Stewart, Timothy A.
 Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
 Ferrara, Napoleone
Filvaroff, Ellen
 Pan, James
Paoni, Nicholas F.
 Kljavin, Ivar J.
Mather, Jennie P.
 APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botsein, David
APPLICANT: Beton, Dan L.
 94; Conservative
 Fong, Sherman
 Stewart, Timod
Tumas, Daniel
 TYPE: PRT
ORGANISM: Homo sapiens
 Best Local Similarity
 GENERAL INFORMATION:
 US-10-706-691-6
 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
 Query Match
 APPLICANT
 Matches
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57 TLRPDYRDRIRLF-ENGSLLLSDLQLADEGTYEVEISIT-DDTFTGEKTINLTVDVPISR 114
 115 POVLV-ASTTVLELSEAFTINCSHENGTKPSYTWIKDGKPLINDSRMLLSPDQKVLTITR 173
 1 VNITSPVRLIHGTVGKSALLSVQYS--STSSDRPVVKWQLKR--DKPVTVVQSIGTEVIG 56
 20 LKVIVPSHIVHGVRGQALYLPVHYGFHTPASDIQII-WLFERPHTMPKYLLGSVNKSVVP 78
 10; Gaps
 Length 450;
 Query Match 25.6%; Score 268; DB 9; Length 450
Best Local Similarity 31.9%; Pred. No. 5.1e-16;
Matches 67; Conservative 43; Mismatches 90; Indels
 197 VTKEDIGNYSCLVRNPVSEMESDIIMPIIY 226
 174 VLMEDDDLYSCMVENPISQGRSLPVKITVY 203
PRIOR PILING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLICATION NUMBER: PCT/US99/21547
PRIOR PELICATION NUMBER: PCT/US99/22089
PRIOR PELING DATE: 1999-11-29
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-06
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-30
PRIOR PLING DATE: 1999-12-30
PRIOR PLING DATE: 1999-12-30
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PRIOR PLING DATE: 1999-12-30
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PRIOR PLING DATE: 1999-12-30
PRIOR PLING DATE: 1999-12-30
PRIOR PLING DATE: 1999-12-30
PRIOR PLING DATE: 1999-12-30
PRIOR PLING DATE: 1999-12-30
 Sequence 320, Application US/09909088B
Patent No. US20020146709A1
GENERAL INFORMATION:
 Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
 Ferrara, Napoleone
Filvaroff, Ellen
 Gerritsen, Mary E
 Gerber, Hanspeter
 Ashkenazi, Avi
Botstein, David
 Fong, Sherman
Gao, Wei-Qiang
 Desnoyers, Luc
Eaton, Dan L.
 APPLICANT: Genentech, Inc
 ; ORGANISM: Homo Sapien
US-09-909-320-320
 Goddard, A
 RESULT 15
US-09-909-088B-320
 APPLICANT:
 APPLICANT:
 APPLICANT
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d
 7;
 57 TLRPDYRDRIRLF-ENGSLLLSDLQLADEGTYEVEISIT-DDTFTGEKTINLTVDVPISR 114
 20 LKVIVPSHTVHGVRGQALYLPVHYGFHTPASDIQII-WLFERFHTMPKYLLGSVNKSVVP 78
 1 VNITSPVRLIHGTVGKSALLSVQYS--STSSDRPVVKWQLKR--DKPVTVVQSIGTEVIG 56
 NPPLICANT: Wood, William, I. Transmembrane Polypeptides and Nucleic ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITLE OF INVENTION: Acids Encoding the Same
 Gaps
 10;
 Length 450;
 Query Match 25.6%; Score 268; DB 9; Length 450 Best Local Similarity 31.9%; Pred. No. 5.1e-16; Matches 67; Conservative 43; Mismatches 90; Indels
 CURRENT APPLICATION NUMBER: US/09/909,088B
CURRENT FILING DATE: 2001-07-18
PRIOR PPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
 PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
WINDER OF SEQ ID NOS: 423
LENGTH: 450
 FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
 FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
 APPLICATION NUMBER: PCT/US99/23089
 APPLICATION NUMBER: PCT/US99/28313
FILING DATE: 1999-11-30
 APPLICATION NUMBER: PCT/US99/28565
FILING DATE: 1999-12-02
 APPLICATION NUMBER: PCT/US99/30095
 APPLICATION NUMBER: US 60/143,048
FILING DATE: 1999-07-07
APPLICATION NUMBER: US 60/145,698
FILING DATE: 1999-07-26
APPLICATION NUMBER: US 60/146,222
FILING DATE: 1999-07-28
 APPLICATION NUMBER: PCT/US99/20594
 PCT/US99/20944
 APPLICATION NUMBER: PCT/US99/28214
 APPLICATION NUMBER: PCT/US99/28564
FILING DATE: 1999-12-02
 APPLICATION NUMBER: PCT/US99/30911
 APPLICATION NUMBER: PCT/US99/30999
 Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
 Nicholas F
 FILING DATE: 1999-09-08
 FILING DATE: 1999-09-15
 FILING DATE: 1999-11-29
 FILING DATE: 1999-12-20
 Roy, Margaret Ann
 FILING DATE: 1999-10-05
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
 APPLICATION NUMBER:
 ILE REFERENCE: 10466-14
 ; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-909-088B-320
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197 VTKEDIGNYSCLVRNPVSEMESDIIMPIIY 226

Search completed: July 26, 2005, 16:21:18 Job time : 52.996 secs

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VLMEDDDLYSCMVENPISQGRSLPVKITVY 203 174

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
```

- protein search, using sw model OM protein July 26, 2005, 15:58:02 ; Search time 11.9615 Seconds Run on:

(without alignments) 1665.085 Million cell updates/sec

US-10-706-691-22

1045 1 VNITSPVRLIHGTVGKSALL......NPISQGRSLPVKITVYRRSS 207 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB 8 Maximum DB 8

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl: \* 2: pir2: \* 3: pir3: \* 4: pir4: \* 4:64 PIR Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|               |       | 40             |        |          | SUMMARIES |                    |
|---------------|-------|----------------|--------|----------|-----------|--------------------|
| Result<br>No. | Score | Query<br>Match | Length | DB       | ID        | Ē,                 |
| -             | 207.5 | 19.9           | 278    | ~        | JC1506    |                    |
| 7             | 207.5 | 19.9           | 341    | ~        | JC1512    |                    |
| ٣             | 202.5 | 19.4           | 278    | ~        | A39037    | carcinoembryonic a |
| 4             | 186   | 17.8           | 458    | <b>?</b> | JC1509    | biliary glycoprote |
| 2             | 181   | 17.3           | 521    | 7        | S34338    | biliary glycoprote |
| 9             | 180.5 | 17.3           | 629    | 7        | A46500    | Ly-9.2 antigen - m |
| 7             | 179.5 | 17.2           | 272    | 7        | 148268    | biliary glycoprote |
| 80            | 179.5 | 17.2           | 278    | ~        | JC1507    | biliary glycoprote |
| 6             | 179.5 | 17.2           | 4      | 7        | JC1511    | biliary glycoprote |
| 10            | 176.5 | 16.9           | 7      | 7        | A54879    | pregnancy-specific |
| 11            | 167   | 16.0           | 853    | 7        | IJBONC    | neural cell adhesi |
| 12            | 166   | 15.9           | 828    | 7        | IJRTNC    | neural cell adhesi |
| 13            | 165   | 15.8           | 7      | ~        | 176668    | pregnancy-specific |
| 14            | 164   | 15.7           | S      | ~        | S68177    | C-CAM2a protein is |
| 15            | 164   | 15.7           | 458    | ~        | S23969    | cell-adhesion mole |
| 16            | 164   | 15.7           | 519    | ~        | A44783    | ecto-ATPase precur |
| 17            | 161   | 15.4           | 458    | ч        | WMMSR1    | biliary glycoprote |
| . 18          | 161   | 15.4           | 521    | 7        | JC1508    | biliary glycoprote |
| 19            | 160.5 | 15.4           | 725    | 7        | JE0100    | neural cell adhesi |
| 20            | 160.5 | 15.4           | 1092   | н        | JN0635    | neural cell adhesi |
| 21            | 159   | 15.2           | 344    | ~        | A27681    | nonspecific cross- |
| 22            | 158.5 | 15.2           | 709    | ~        | A35364    | carcinoembryonic.a |
| 23            | 157   | 15.0           | 299    | 7        | S56749    | junctional adhesio |
| 24            | 156.5 | 15.0           | 761    | н        | IJHUNG    | neural cell adhesi |
| 25            | 155   | 14.8           | 324    | ~        | G43354    | pregnancy-specific |
| 26            | 155   | •              | ~      | ~        | F43354    | pregnancy-specific |
| 27            | 155   | 14.8           | n      | ~        | A43354    | pregnancy-specific |
| 28            | 155   | 14.8           | 335    | ~        | m         | pregnancy-specific |
| 53            | 155   | 14.8           | 395    | ~        | D43354    | pregnancy-specific |

| pregnancy-specific | pregnancy-specific<br>pregnancy-specific | pregnancy-specific | pregnancy-specific | pregnancy-specific | pregnancy-specific | pregnancy-specific | pregnancy-specific | neural cell adhesi | neural cell adhesi | biliary glycoprote | biliary glycoprote | biliary glycoprote | biliary glycoprote | pregnancy-specific |
|--------------------|------------------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| C43354             | A28277                                   | A33258             | A31135             | A35964             | B33258             | A35341             | A27658             | JE0099             | LJCHNL             | A40305             | JH0395             | JH0396             | JH0394             | B54312             |
| 20                 | N 64                                     | 7                  | N                  | ~                  | ~                  | 7                  | N                  | 7                  | -                  | 7                  | N                  | ~                  | ~                  | 7                  |
| 397                | 417                                      | 419                | 419                | 426                | 426                | 426                | 428                | 725                | 1091               | 206                | 321                | 351                | 417                | 419                |
| 14.8               | 14.8                                     | 14.8               | 14.8               | 14.8               | 14.8               | 14.8               | 14.8               | 14.8               | 14.8               | 14.7               | 14.7               | 14.7               | 14.7               | 14.7               |
| 155                | 155                                      | 155                | 155                | 155                | 155                | 155                | 155                | 154.5              | 154.5              | 154                | 154                | 154                | 154                | 154                |
| 30                 | 32                                       | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

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A; A; Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopro A; A; Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopro A; A; Accession: JCL506
A; A; Accession: JCL506
A; Status: nucleic acid sequence not shown
A; Molecule type: A,Residues: 1-278 mac. A,Residues: 1-278 mac. A,Residues: 1-278 mac. A,Residues: 1-278 mac. A,Residues: 1-278 mac. A,Residues: 1-278 mac. A,Residues: UNIPROT:099232
C,Comment: This protein is expressed at the cell surface and plays a determinant role in C,Genetics: A,Gene: Bgp8
C,Superfamily: biliary glycoprotein; carcinoembryonic antigen precursor amino-terminal homology cCEAN> F;1-138/Domain: arcinoembryonic antigen precursor amino-terminal homology cCEAN> F;159-216/Domain: immunoglobulin homology cIMM> F;87,104,153,195/Binding site: carbohydrate (Asn) (covalent) #status predicted biliary glycoprotein B - mouse C;Species: Mus musculus (house mouse) C;Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 09-Jul-2004 C;Accession: JCISO6 E;Accusig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N. Gene 127, 173-183, 1993

95 40 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITD Gaps . ن Length 278; Query Match
19.9%; Score 207.5; DB 2; Length
Best Local Similarity 32.1%; Pred. No. 3.5e-09;
Matches 54; Conservative 32; Mismatches 73; Indels

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DTF-TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPL 154 δ g

155 LNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITV 202 QLTERMTLSQNNSILRIDPIKREDAGEYQCRISNPVSVKRSNSIKLDI 232 185 셤 ò

RESULT 2

JC1512
Liliary glycoprotein.H - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 09-Jul-2004
C;Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 09-Jul-2004
C;Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 09-Jul-2004
C;Date: 24-Feb-1993 M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
A;Title: Expression of the Bgp gene and characterization of mouse colon biliary glycoproidate and characterization of mouse colon biliary glycoproidate A;Accession: JC1512

```
biliary glycoprotein F - mouse
 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-521 <HUA>
 A; Accession: JC1510
 A; Accession: A41093
 187
 C,Genetics:
A,Gene: BgpE
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Matches
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 A39037
Carcinocembryonic antigen mmCGM2 precursor - mouse
NyAlternate names: bilary glycoprotein homolog; calcium-dependent cell adhesion molecul
C;Species: Mus musculus (house mouse)
C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 09-Jul-2004
C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 09-Jul-2004
C;Accession. 266, 309-315, 1991
A;Turbide, C.; Rojas, M.; Stanners, C.P.; Beauchemin, N.
J. Biol. Chem. 266, 309-315, 1991
A;Turbide, C.; Rojas, M.; Stanners, C.P.; Beauchemin, N.
A;Turbide, C.; Rojas, M.; Stanners, C.P.; Beauchemin, N.
A;Accession: A39037; MuID:91093141; PMID:1985902
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A;Accession: A39037; MuID:91093141; PMID:1985902
A;Accession: Biologic A;TURA
A;Residues: 1-278
A;Accession: A39037
A;Accession: A39037
A;Accession: Biologic A;Allar
A;Residues: 1-278
A;Accession: A39037
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A;Accession: A39037
A;Accession: A39037
A;Accession: A39037
A;Accessio
A; Molecule type: mRNA
A; Residues: 1-341 <MCC>
A; Cross-references: UNIPROT: Q61354; GB: X67283
C; Comment: This protein is expressed at the cell surface and plays a determinant role in
C; Genetics:
A; Gene: BgpH
C; Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C; Reywords: glycoprotein; receptor
C; Reywords: glycoprotein; receptor
F; 1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F; 159-216/Domain: immunoglobulin homology <IMM>
F; 159-216/Domain: immunoglobulin homology <IMM>
F; 87, 104, 153, 195/Binding site: carbohydrate (Asn) (covalent) #status predicted
 5
 : ||: | : | | : | : | | | : | : | | | : | | : | | | : | | | : | : | | | : | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
 : | | | : : | | : : | | : : | | | ENFRETEATIVOFHUNDOPYTOPSLOVITITYVKEL-DSUTLICL-SNDIGANIQWLFNSQSL 184
 DTF-TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPL 154
 96 DTF-TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPL 154
 : | | : | | : : | : : | : : | 184
 40 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITD 95
 40 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITD 95
 Gaps
 Gaps
 9
 OLTERMILISONNSILRIDPIKREDAGEYQCEISNPVSVKRSNSIKLDI 232
 LNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITV 202
 DB 2; Length 278;
 155 LNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITV 202
 DB 2; Length 341;
 | | | | : : | | : | | : | | : | | : | | | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
 73; Indels
 74; Indels
 19.9%; Score 207.5; DB 2, 32.1%; Pred. No. 4.6e-09; tive 32; Mismatches 73,
 Query Match 19.4%; Score 202.5; DB 2 Best Local Similarity 32.1%; Pred. No. 8.8e-09; Matches 54; Conservative 31; Mismatches 74
 54; Conservative
 Query Match
Best Local Similarity
 96
 127
 185
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C.Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terming C.Superfamily: carcinoembryonic antigen precursor amino-terminal dycoprotein; receptor F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>F;160-219/Domain: immunoglobulin homology <IMMI>F;254-303/Domain: immunoglobulin homology <IMMI>F;339-396/Domain: immunoglobulin homology <IMMI>F;87,104,148,199,206,210,226,258,290,294,304,333,375/Binding site: carbohydrate (Asn) (cc)
 A;Cross-references: UNIPROT:061352; EMBL:X67281; NID:g312585; PIDN:CAA47698.1; PID:g31258; R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N. Gene 127, 173-183, 1993
A;Title: Expression of the Bap gene and characterization of mouse colon biliary glycoprot A;Reference number: JC1505; MUID:93273228; PMID:8500759
 A,Molecule type: mRNA
A,Rebidues: 1-81, V.Q.,83-141, P',143-521 <MCC>
A,Cross-references: GB:K67281
R,Williams, R.K.; Jiang, G.S.; Holmes, K.V.
R,Williams, R.K.; Jiang, G.S.; Holmes, K.V.
A,Title: Receptor for mouse hepatitis virus is a member of the carcinoembryonic antigen f
A,Reference number: A41093; MUID:91288498; PMID:1648219
 Rinctuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N. Gene 127, 173-183, 1993
A;Title: Expression of the Bgp gene and characterization of mouse colon biliary glycoprot A;Title: Expression of 501505; MUD:93273228; PMID:8500759
A;Reference number: JC1505, MUD:93273228; PMID:8500759
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-458 <MCC>
A;Cross-references: UNIPROT:Q61351; GB:X67280
C;Comment: This protein is expressed at the cell surface and plays a determinant role in
 NyAlternate names: mouse hepatitis virus (WHV) receptor glycoprotein C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Accession: 20-Feb-1995 #sequence revision 20-Feb-1995 #sequence revision 20-Feb-1995 #sequence revision 20-Feb-1995 #sequence revision 234338; UCIS10; A4093 R;Huang, D.C.; Huang, X.F.; Novel, M.; Novel, G. Submitted to the EMBL Data Library, July 1992 Submitted to the EMBL Data Library, July 1992 A;Reference number: S34338
 96 DTF-TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNC-SHENGTKPSYTWLKDGKP 153
C;Species: Mus musculus (house mouse)
C;Date: 24-Peb-1994 #sequence_revision 24-Peb-1994 #text_change 09-Jul-2004
C;Accession: JC1509
 40 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITD
 .;
6
 154 LLNDSRMLLSPDQKVIJITRVLMEDDDLYSCMVENPISQGRSLPVKITV 202
 Length 458;
 Indels
 79;
 Match 17.8%; Score 186; DB 2; Local Similarity 27.8%; Pred. No. 3.4e-07; les 47; Conservative 35; Mismatches 79.
 A;Status: preliminary
A;Molecule type: protein
A;Residues: 35-59 <WIL>
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 RESULT 6
A46500
Cy 2 antigen - mouse
Cy 5pecies: Wus musculus (house mouse)
Cy 5pecies: Wus musculus (house mouse)
Cy 5pecies: Wus musculus (house mouse)
Cy 5pecies: Mus musculus
Cy 5pecies: Mus musculus
Cy 5pecies: Musunol. 149, 1636-1641, 1992
Ay Title: Isolation and characterization of cDNA clones for mouse Ly-9.
Ay Feference number: A46500, MUD: 92373005; PMID: 1506686
Ay Accession: A46500
Ay Status: preliminary
Ay Molecule type: mRNA; protein
Ay Residues: 1-629 < SAN>
Ay Residues: 1-629 < SAN>
Ay Corserved: Musculus (BS M84412; NID: 9198931; PIDN: AAA39468.1; PID: 9198932
Ay Experimental source: C57BL/6
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 amino-termir
C;Comment: This protein is expressed at the cell surface and plays a determinant role G;Genetics:
A;Gene: BapF
S;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-term C;Keywords: glycoprotein; receptor
F;11-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>F;160-219/Domain: immunoglobulin homology <IMM1>F;264-303/Domain: immunoglobulin homology <IMM2>F;339-396/Domain: immunoglobulin homology <IMM3>F;319-396/Domain: immunoglobulin homology <IMM3>F;87,104,148,199,206,210,226,258,290,294,304,333,375/Binding site: carbohydrate (Asn)
 7;
 DTF-TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNC-SHENGTKPSYTWLKDGKP 153
 RIRLFENG-SLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVASTT 123
 124 VLEL-SEAFTLNCSHENGTKPS--YTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 BSDIDSCTFTLICT-VKGTKDSVQYSWTRE-----DTHLNTYDGSHTLRVSQSVCDPDL 197
 95
 SPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRD 64
 148268
biliary glycoprotein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 40 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITD
 Note: sequence extracted from NCBI backbone (NCBIN:111651, NCBIP:111654)
 Gaps
 8
 LSEGDŘLKLSEGNRTLTLLNÝTRNĎTGPÝVČETRNPVSVNŘSDPFSLNI 235
 LLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITV 202
 Length 629;
 Length 521;
 17.3%; Score 181; DB 2; Length 52:
27.8%; Pred. No. 1e-06;
wiematches 80; Indels
 Indels
 DB 2;
 Query Match 17.3%; Score 180.5; DB 2 Best Local Similarity 27.5%; Pred. No. 1.4e-06; Matches 55; Conservative 40; Mismatches 90
 LYSCMVENPISOGRSLPVKI 200
 PYTCKAWNPVSQNSSQPVRI 217
 A;Note: sequence extractor C;Keywords: transmembrane protein
 Best Local Similarity 27.8
Matches 47; Conservative
 69
 127
 'n
 65
 85
 145
 96
 154
 Query Match
 187
 RESULT 7
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C; Accession: 148268
Nivedallec, P.; Duckaler, G.S.; Daniels, B.; Turbide, C.; Chow, B.; Basile, A.A.; Holmes J. Virol. 68, 4525-4537, 1994
A; Title: Bgp2, a new member of the carcinoembryonic antigen-related gene family, encodes A; Reference number: A53995; MUID:94267915; PMID:8207827
A; Accession: 148268
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-272 cRES
A; Cross-references: UNIPROT: QBRINS; EMBL: X76085; NID:9511020; PIDN:CAA53699.1; PID:95110
 biliary glycopro-
 A, Accession: JC1507
A, Molecule type: mRNA
A, Residues: 1-278 «MCC>
A, Cross-references: UNIPROT: Q61350; GB: X67278
C; Comment: This protein is expressed at the cell surface and plays a determinant role in
 C; Superfamily: biliary glycoprotein; carcinoembryonic antigen precursor amino-terminal Keywonds: glycoprotein at Keywords: glycoprotein carcinoembryonic antigen precursor amino-terminal homology <CEAN> F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN> F;159-216/Pomain: immunoglobulin homology <IMM>
 C, Superfamily: biliary glycoprotein; carcinoembryonic antigen precursor amino-terminal C; Keywords: glycoprotein; receptor C; Keywords: glycoprotein; receptor P; P; 1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN> F; 75-124/Domain: immunoglobulin homology <IMM1> F; 159-216/Domain: immunoglobulin homology <IMM2> F; 159-216/Domain: immunoglobulin homology <IMM2> F; 1189-104, 153, 195/Binding site: carbohydrate (ABn) (covalent) #status predicted
 111
 --GPVHSGRETLYSNGSLLIQRVTMKDTGVYTIE--MTDQNYRRRVLTGQ----FHVHKP 143
 144 VIQPSLQVINTIVKEL-DSVILICISKD-RQAHIHWIFNNDTLLITEKMITSQAGLILKI 201
 112 ISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTI 171
 62 YRDRIRLFENGSLILLSDLQLADEGTYEVEISITDDTF-TGEKTINLTVDVPISRPQVLVA 120
 95 YSGREIIYSNGSLLFQMITMKDMGVYTLD--MTDENYRRTQATVRFHVHQPVTQPFLQVT 152
 STTVLELSEAFILNCSHENGTKPSYTWLKDGKPLLNDSRWLLSPDQKVLTITRVLMEDDD 180
 99
 91
 biliary glycoprotein C - mouse
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
 57 TLRPDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTF-----TGEKTINLTVDVP
 10 IHGTVGKSALLSV------QYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIG
 mouse colon
 C;Accession: JC1507
R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin,
Gene 127, 173-183, 1993
 39;
 ..
21
 Length 278;
 Length
 77; Indels
 Indels
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 Gene 127, 173-183, 1993
A;Title: Expression of the Bgp gene and characterization
A;Reference number: JC1505; MUID:93273228; PMID:8500759
 DB 2;
 17.2%; Score 179.5; DB 2; ilarity 31.7%; Pred. No. 5.8e-07; Conservative 29; Mismatches 63;
 17.2%; Score 179.5; DB 2, 26.1%; Pred. No. 5.7e-07; tive 40; Mismatches 77
 DPIKREDAGEYQCEISNPVSVKRSNSIKLEV 232
 172 TRVLMEDDDLYSCMVENPISQGRSLPVKITV 202
 Conservative
 Query Match
Best Local Similarity
....hes 45; Conserva
 Query Match
Best Local Similarity
Matches 55; Conserv
 121
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NiAlternate names: NCAM-140
Cispecies: Bos primigenius taurus (cattle)
Cipate: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
CiAccession: A32976; A38778; B44290; S05402
Rilipkin, V.M.; Khramtsov, N.V.; Andreeva, S.G.; Moshnyakov, M.V.; Petukhova, G.V.; Rakit, PESS Lett. 254, 69-73, 1989
A;Title: Calmodulin-independent bovine brain adenylate cyclase. Amino acid sequence and mark alserence number: A32976; MUID:89378239; PMID:2776887
 A; Molecule type: protein
A; Residues: 20-35;51-61;113-117;122-147;155-161;262-275;279-302;353-360;369-382;544-562;6
A; Residues: 20-35;51-61;113-117;122-147;155-161;262-275;279-302;353-360;369-382;544-562;6
B; Note: the authors identified this protein as calmodulin-independent adenylate cyclase
B; Rougon, G.; Marshak, D.R.
J. Biol. Chem. 261, 3396-3401, 1986
A; Title: Structural and immunological characterization of the amino-terminal domain of many R; Reference number: A44290; MUID:86140120; PMID:3512556
 A;Recaldues: 20-36 -ROU>
A;Recaldues: 20-36 -ROU>
A;Recaldues: 20-36 -ROU>
A;Residues: 20-36 -ROU>
A;Residues: 20-36 -ROU>
A;Residues: 20-36 -ROU>
A;Rocte: 20-36 -ROU>
A;Rocte: 20-36 -ROU>
A;Rocte: 20-36 -ROU>
C;Comment: Natious forms of NCAM are produced by alternative splicing.
C;Comment: Natious forms of NCAM are produced by alternative splicing.
C;Comment: Natious forms of NCAM are produced by alternative splicing.
C;Comment: Nations of NCAM are produced by alternative splicing.
C;Comment: Splicing: Parain; cell adhesion molecule, fibronectin type III repeat homology; immunc;
C;Reywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; sie;
F;20-85;Product: neural cell adhesion molecule, short domain form #status experimental r;
F;20-85;Product: neural cell adhesion molecule, short domain form #status experimental r;
F;20-85;Product: neural homology <IMM1>
F;20-85;Product: neural homology <IMM2>
F;161-165;Region: heparin binding #status predicted
F;21-156;Region: heparin binding #status predicted
F;21-270;Region: NCAM binding #status predicted
F;21-396;Domain: immunoglobulin homology <IMM3>
F;22-490;Domain: immunoglobulin homology <IMM3>
F;22-64,Domain: immunoglobulin homology <IMM3>
F;22-64,Domain: immunoglobulin homology <IMM3>
F;22-64,Domain: intransembrane #status predicted <IMM>
F;22-737/Domain: intrancellular #status predicted <IMM>
F;22-731/Domain: intrancellular #status predicted <IMM>
F;22-731,314,335-386,328-3384,435-4488/Disulfide bonds: #status predicted
F;22-314,346,432,458,487/Binding site: carbohydrate (Asn) (covalent)
 A; Molecule type: mRNA
A; Residues: 1-853 <LIP>
A; Cross-references: UNIPROT: P31836; GB: X16451; NID: g60; PIDN: CAA34470.1; PID: g61
A; Accession: A38778
 7
 884 HAVEGESVLLYVH--NLPEALQTFSWYKGVYSLKEFK--IAEYSIATKSVFP-GPAHKGR 338
 124
 : ||||||||| || || : :: :: :: || || : || : || 399 ATGYINGSILLQDLTARDTGLYTL-VTLDSNSKIKSAPVQVTVHKPVTQPFLRVTESTVT 397
 143 SSLPPTIIWKHK------GRDVI--LKKDV--RFIVLTNNYLQIRGIKKTDEGTY 187
 125 LELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSC 184
 398 VOSSVVFT -- CLSDN - TGVSIRWLFKNONLQVTERMTLSPSNCQLRIHDVRREDAGQYRC 454
 87
11 HGTVGKSALLSVQYSSTSSDRPVVKW-----QLKRDKPVTVVQSIGTEVIGTLRPDYRDR
 66 IRLFENGSLILSDLOLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTV-
 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY
 Gaps
 neural cell adhesion molecule short domain form precursor - bovine
 16.0%; Score 167; DB 1; 30.9%; Pred. No. 2.4e-05; ive 28; Mismatches 73;
 185 MVENPISQGRSLPVKITV 202
 455 EAFNPISSKTSRPVSLAV 472
 Conservative
 Local Similarity
nes 55; Conserv
 A; Accession: B44290
 A;Accession: A32976
 Query Match
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 Pregnancy-specific glycoprotein rnCGM3 - rat
C;Speciaes: Rattus norvegicus (Norway rat)
C;Speciaes: Rattus norvegicus (Norway rat)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
C;Accesion: A54879
R;Chen, C.L.; Chou, J.Y.
Biochemistry 33, 9615-9626, 1994
A;Title: Characterization of two promoters of a rat pregnancy-specific glycoprotein gene
A;Reference number: A54879; MUID:94347731; PMID:8068638
A;Accession: A54879
A;Retus: prelliminary
A;Molecule type: DNA
A;Retus: prelliminary
A;Molecule type: DNA
A;Retus: prelliminary
A;Molecule type: DNA
A;Retus: prelliminary
A;Note: authors translated the codon GCT for residue 64 as Gly
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C;Keywords: glycoprotein
C;Keywords: glycoprotein
F;1-137/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA1>
F;242-378/Domain: carcinoembryonic antigen precursor amino-terminal inmunoglobulin homology <IMM2>
 A; Wolecule type: DNA
A; Residues: 1-341 <MCC>
A; CROSS-references: UNIPROT: Q61353; GB: X67282
C; Comesent: This protein is expressed at the cell surface and plays a determinant role in
C; Genetics: A; Gene: BgpG
C; Genetics: BgpG
C; Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C; Keywords: Glycoprotein; receptor
C; Keywords: Glycoprotein; receptor
F; F; 1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F; F; 1-128/Domain: immunoglobulin homology <IMM1>
F; F; 1-218/Domain: immunoglobulin homology <IMM1>
F; F; 1-218/Domain: immunoglobulin homology <IMM1>
F; F; 1-218/Domain: immunoglobulin homology <IMM2>
F; T; 1,89,104,153,195/Binding site: carbohydrate (Asn) (covalent) #status predicted
 JC1511

JC1511

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JC1511

G. Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Ju1-2004

C. Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Ju1-2004

C. Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Ju1-2004

R. McCataig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.

Gene 127, 173-183, 1993

A. Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopro

A. Reference number: JC1505; MUID:93273228; PMID:8500759
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 4
 62 YRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTF-TGEKTINLTVDVFISRPQVLVA 120
 YSGREIIYSNGSLLFOMIIMKDMGVYTLD--MTDENYRRTQATVRFHVHQPVTQPFLQVT 152
 : | | | | : : | | | : : | | | : : | | | : : | | | | | : : | | | | : : | | | | : : | | | : : | | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | : | : | : | : | : | : | : | : : | : | : | : : | : | : : | : | : | : : | : | : | : : | : | : : | : | : : | : | : : | : | : : | : | : | : : | : | : : | : | : |
 121 STIVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDOKVLTITRVLMEDDD 180
 Gaps
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 15;
 16.9%; Score 176.5; DB 2; Length 475; Llarity 32.3%; Pred. No. 2e-06; Conservative 24; Mismatches 95; Indels 15
 ch 17.2%; Score 179.5; DB 2; Length 341; Similarity 31.7%; Pred. No. 7.6e-07; 45; Conservative 29; Mismatches 63; Indels 5
 211 EYQCEISNPVSVRRSNSIKLDI 232
 211 EYQCEISNPVSVRRSNSIKLDI 232
 181 LYSCMVENPISQGRSLPVKITV 202
 LYSCMVENPISQGRSLPVKITV 202
 Query Match
Best Local Similarity
Matches 64; Conserva
 Query Match
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C;Accession: S68177
R;Lucka, L.; Cichocka, I.; Baeumler, K.; Bechler, K.; Reutter, W.
R;Lucka, L.; Cichocka, I.; Baeumler, K.; Bechler, K.; Reutter, W.
Biochem. 234, 527-535, 1995
A;Title: A short isoform of carcinoembryonic-antigen-related rat liver cell-cell adhesio A;Reference number: S68177; MUID:96128184; PMID:8536699
A;Accession: S68177
 Cross-references: UNIPROT:063093; EMBL:X91137; NID:g1160272; PIDN:CAA62577.1; PID:g1160; Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA>
 C; Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
 A;Cross-references: UNIPROT:Q62056; GB:M83344; NID:g200316; PIDN:AAA39916.1; PID:g200317
 R;Rudert, F.; Saunders, A.M.; Thompson, J.A.; Rebstock, S.; Zimmermann, W.A. Mamm. Genome 3, 262-273, 1992
A;Title: Characterization of murine carcinoembryonic antigen gene family members. A;Reference number: 157007; MUID:92345715; PMID:1638085
 <CEA1>
 S,
 5
 376
 EVEISITIDIFFIGEKTINLTVDVP--ISRPQVLVASTTVLELSEAFTLNCSHENGTKPSY 145
 --- DSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPI-SQGRSLPVKI 200
 106
 pregnancy-specific glycoprotein - mouse
C;Species: Mus muscullus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I76668
 C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C;Keywords: glycoprotein
F;1-137/Domain: carcinoembryonic antigen precursor amino-terminal homology
F;399-456/Domain: immunoglobulin homology <IMM>
 |:| :: |:|: || || || || 377 QVNVHKLATQPVIKATDSTVRVQGSVIFTCFSDN-TGVSIRWLFNNQRLQLTERMTLSPS
 49 SIGTE--VIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINL
 107 TVDV-PISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPD
 Gaps
 Gaps
 10;
 5,
 Fi-33/Domain: signal sequence #status predicted <SIG>
F;34-458/Product: C-CAMZa protein isoform #status predicted <MAT>
F;252-301/Domain: immunoglobulin homology <IMM>
 Length 475;
 Length 458;
 69; Indels
 61; Indels
 15.8%; Score 165; DB 2; llarity 33.1%; Pred. No. 1.6e-05; Conservative 26; Mismatches 69;
 ch 15:7%; Score 164; DB 2; 1 Similarity 32.6%; Pred. No. 1.9e-05; 42; Conservative 24; Mismatches 61
 166 QKVLTITRVLAMEDDDLYSCMVENPISQGRSLPVKITV
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 C-CAM2a protein isoform precursor - rat
 146 TWLKDGKPLLN-
 Query Match
Best Local Similarity
Matches 52; Conserv
 Query Match
Best Local Similarity
 A; Residues: 1-475 < RES>
 A; Residues: 1-458 < LUC>
 A;Status: preliminary
A;Molecule type: mRNA
 A, Accession: I76668
 A; Molecule type:
 88
 436
 A; Gene: CGM5
 C;Genetics:
 Matches
 RESULT 14
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1,07870 eal adhesion molecule short domain form precursor - rat

1,07870 eal adhesion molecule short domain form precursor - rat

1,07870 eal sep-1991 When-tau novegled to When-tau novegled
 7;
 EVEISITDDTFTGEKTINLTVDVP--ISRPQVLVASTTVLELSEAFTLNCSHENGTKPSY 145
 RCEGRILARGEINFKDIQVIVNVPPTVQARQSIVNATA--NLGQSVTLVCNAEGFPEPTV 245
 -----GRDVI--LKKDV--RFIVLSNNYLQIRGIKKTDEGTY 187
 TWLKDGKPLLN--DSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPI-SQGRSLPVKI 200
 28 SSDRPVVKWOLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY
 24;
 Length 858;
 74; Indels
 15.9%; Score 166; DB 1; 30.0%; Pred. No. 2.9e-05; ive 28; Mismatches 74;
 Conservative
 143 SSLPPTIIWKHK---
 Similarity
 54;
 Query Match
Best Local S
Matches 54
88
 188
 146
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completed: July 26, 2005, 16:14:16 is: 12.9615 secs
194 RSLPVKITV 202
 402 ISHPIKLDV 410
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 Call-adhesion molecule short form (cell-CAM105) - rat

call-adhesion molecule short form (cell-CAM105) - rat

N;Alternate names: C-CAM protein

C;Species: Rattus norvegicus (Norway rat)

C;Date: 22-Nov-1993 #sequence revision 01-Sep-1995 #text_change 09-Jul-2004

C;Date: 22-Nov-1993 #sequence revision 01-Sep-1995 #text_change 09-Jul-2004

C;Date: 22-Nov-1993 #sequence revision 01-Sep-1995 #text_change 09-Jul-2004

C;Date: 22-Nov-1993 #sequence revision 01-Sep-1995 #text_change 09-Jul-2004

C;Date: 22-Nov-1993 #sequence revision 01-Sep-1995 #text_change 09-Jul-2004

R;Cullic, O.; Huang, Q.H.; Flanagan, D.; Hixson, D.; Lin, S.H.

A;Title: Molecular cloning and expression of a new rat liver cell-CAM105 isoform. Differ A;Reference number: S23969; MUID:92344597; PMID:1637321

A;Receion: S23969

A;Residues: 1-458 <CULL NO CONSET REPRESSION NO CAMPROSEN PROPERSOR A;Redidues: 1-458 <CULL NO CONSET REFERENCE NO CAMPROSEN PROPERSOR R;Rediund, M.; Gaardsvoll, H.; Book, E.; Ochrink, B.

Eur. J. Biochem. 213, 1109-1116, 1993

Eur. J. Biochem. 213, 1109-1116, 1993
 A;Accession: S10563
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Residues: "X',58-66,"A',68,121-124,"F',126,"Q',128-134,"X',136-138,"X',356-360,"X',362
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F;357-394/Domain: immunoglobulin homology <IMM3>
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A;Status: preliminary
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A;Molecule type: mRNA
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A;Cross-references: EMBL:X71122; NID:g287819; PIDN:CAAS0435.1; PID:g287820
A;Cross-references: EMBL:X71122; NID:g287819; R.; Thompson, N.; Hixson, D.C.; Lin, S.H.
Biochem. J. 295, 427-435, 1993
A;Title: The cytoplasmic domain of C-CAM is required for C-CAM-mediated adhesion functic
A;Reference number: S38826; MUID:94058980; PMID:8240240
A;Status: preliminary
 A;Title: Different isoforms and stock-specific variants of the cell adhesion molecule C-
A;Reference number: S32483; MUID:93279310; PMID:8504806
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A,Cross-references: EMBL:M92848; NID:g203366; PIDN:AAA16783.1; PID:g203367
R;Aurivillius, M.; Hansen, O.C.; Lazrek, M.B.S.; Bock, E.; Oebrink, B.
 FEBS Lett. 264, 267-269, 1990
A;Title: The cell adhesion molecule cell-CAM 105 is an ecto-ATPase and a member of the
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 42; Conservative
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 402 ISHPIKLDV 410
 Query Match
Best Local Similarity
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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| 116.1<br>116.0<br>116.0<br>116.0<br>116.0<br>116.0<br>116.0<br>116.0<br>116.7                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |            | PRELIMINARY          | (TrEMBLrel.<br>(TrEMBLrel.<br>(TrEMBLrel.<br>protein.                                                                                 | ; Metazoa;<br>Eutheria;<br>D=9606;                                                                  | N. N. A.                           | M.C.;<br>ted to ]<br>UL-2001)                                                                                                                                  | R003599<br>R007110                        | 7; 1g;<br>09; 1G;<br>08; 1GC;<br>0835; 1C<br>proteir               | larity<br>Conserva                                                                                               | SPVRLIE                                                         | RSPVRLI                                                      | ORIRLFER<br>       <br>ORIRLFER                                  | TELSEA!                                                              | CMVENPIS                            |
| 166<br>166<br>166<br>166<br>166<br>166<br>166<br>166<br>166<br>166                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |            |                      | 25-0CT-2004<br>25-0CT-2004<br>25-0CT-2004<br>25-0CT-2004<br>Hypothetical                                                              | Eukaryota; Metaz<br>Bukaryota; Metaz<br>Mammalia; Euther<br>NCBI_TaxID=9606;                        | SEQUENCE FROM N.A<br>TISSUE-Liver; | en S., Mon<br>gene relat<br>bmitted (JT<br>BT,: AY0475                                                                                                         | terPro; IPI<br>terPro; IPI<br>terPro; IPI | ART; SMO04<br>ART; SMO04<br>ART; SMO04<br>OSITE; PSS<br>pothetical | Match<br>Local Similarity 100<br>Les 207; Conservative                                                           | 1 VNIT                                                          | 34 VNI                                                       | 61 DYRI<br>    <br>94 DYRI                                       | 121 STTV<br>    <br>154 STTV                                         | 181 LYSC<br>    <br> 214 LYSC       |
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416 AA.

PRT;

PRELIMINARY;

Q8N713 ID Q8N713 AC Q8N713;

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Q6van8 Q9nx42 Q96iq7

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RESULT 2

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Matsumura Y., Moriya S., Chiba E., Momiyama H., Onogawa S.,
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Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y.,
Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K.,
Kanehori K., Takahashi-Pujii A., Oshima A., Sugiyama A., Kawakami B.
Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
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17-JUL-2004 (TrEMBLrel.)
17-JUL-2004 (TrEMBLrel.)
17-JUL-2004 (TrEMBLrel.)
17-JUL-2004 (TrEMBLrel.)
17-JUL-
 TISSUE-Brain;
TISSUE-Brain;
TISSUE-Brain;
Fukuzumi Y., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
Fukuzumi Y., Fujimori Y., Komiyama M., Suzuki Y., Hata H.,
Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami
Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami
Sugai K., Isogai T., Sugano S.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO98396; BAC05297.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig-c2.
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 ö
 99.6%; Score 1041; DB 2; Length 416; 99.5%; Pred. No. 8e-74; ive 1; Mismatches 0; Indels (
 PS50835; IG_LIKE; 1.
416 AA; 45994 MW; 47120CA9A00EEICF CRC64;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
101-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein FL725530.
Homo sapiens (Human).
 367 AA
 181 LYSCMVENPISQGRSLPVKITVYRRSS 207
 PRT;
 Conservative
 Pfam; PF00047; ig; 1.
SMART; SM00408; IGC2; 1.
 PRELIMINARY;
 Local Similarity
les 206; Conserv
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 NCBI_TaxID=9606;
 121
 SEQUENCE
 PROSITE;
 Query Match
 D6ZWL4
 Matches
 RESULT 3
QGZWL4
AC QGZW
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DD QGZW
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SEQUENCE FROM N.A.

STRAIN=C57BL/6; TISSUE=Brain;
STRAIN=C57BL/6; TISSUE=Brain;
STRAIN=C57BL/6; TISSUE=Brain;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buercow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buercow K.H., Schaefer C.F., Bhat N.K.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casrvint T.L., Scheetz T.E.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley W.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Generation and initial analysis of more than 15,000 full-length human
 ö
 61 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 120
 94 DSRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVFISRPQVLVA 153
 121 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 9
 93
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 14 VNITSPVRLIHGITUGERSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 Gaps
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ö
 98.8%; Score 1032; DB 2; Length 367; 99.0%; Pred. No. 3.5e-73; tive 1; Mismatches 1; Indels (
 Receptor.
SEQUENCE 367 AA; 40456 MW; 35956FA245A408F0 CRC64;
 25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
2900042E01Rik protein (Fragment).
 roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
 413 AA
EMBL, AK122595, BAC85486.1, -.. GO, GO:0004872; F:receptor activity; IEA. InterPro; IPR003599; Ig. InterPro; IPR003599; Ig. InterPro; IPR007110; Ig-like. InterPro; IPR007598; Ig_c2. SMART; SM00409; IG; 2. SMART; SM00409; IGc2; 1. PROSITE; PS50835; IG_LIKE; 1.
 214 LYSCVVENPISOGRSLPVKITVYRRSS 240
 LYSCMVENPISQGRSLPVKITVYRRSS 207
 PRT;
 [2]
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
 and mouse cDNA sequences."
 Best_Local Similarity 99.09
Matches 205; Conservative
 PRELIMINARY;
 NCBI_TaxID=10090;
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57 TLRPDYRDRIRLF-ENGSLLLSDLQLADEGTYEVEISIT-DDTFTGEKTINLTVDVPISR 114
 Created)
Last sequence update)
Last annotation update)
 174 VLMEDDDLYSCMVENPISQGRSLPVKITVY 203
 278 AA
 341 AA
 197 VTKEDIGNYSCLVRNPVSEMESDIIMPIIY
 (TrEMBLrel. 01, Created)
 PRT;
 35 278 P
 HSSP, Q61353; 1L6Z.
MGD; MGI:1347245; Ceacaml.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
 Pfam; PF00047; ig; 1.
SMART; SM00408; IGc2; 1.
PROSITE; PS50835; IG_LIKE; 1.
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 (TrEMBLrel. (TrEMBLrel. (TrEMBLrel. (TrEMBLrel. 2)
 PRELIMINARY;
 PRELIMINARY;
 PIR; A39037; A39037.
PIR; JC1506; JC1506.
 Mus musculus (Mouse)
 Q61354;
01-NOV-1996
01-NOV-1996
01-OCT-2003
 01-NOV-1996
 CHAIN
SEQUENCE
 115
 Q99232
ID Q99232
 SIGNAL
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 Q61354
ID Q6
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 208
 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 9
 29 VNITSPVRLIHGTVGKSALLSVQYSSTSSDKPVVKWQLKRDKPVTVVQSIGTEVIGTLRP 88
 20 LKVTVPSHTVHGVRGQALYLPVHYGFHTPASDIQII-WLFERPHTMPKYLLGSVNKSVVP 78
 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD
 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 DYRDRIRLFENGSLLLSDLQLADECTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA
 MEDLINE-22887296; PubMed=12975309; DOI=10.1101/gr.1293003; MEDLINE-22887296; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya B., Baker K., Baldwin D., Brush J., Chow B., Chui C., Crowley C., Currell B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmon L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 1 VNITSPVRLIHGTVGKSALLSVQYS--STSSDRPVVKWQLKR--DKPVTVVQSIGTEVIG
 Gaps
 "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: bioinformatics assessment.";
bioinformatics assessment.";
Genome Res. 13:2265-2270(033).
EMBL; AY358345; AAQ8711.1; -..
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig-like.
InterPro; IPR003598; Ig-22.
Pfam; PF00047; ig; 1.
 Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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 10;
 98.5%; Score 1029; DB 2; Length 413; 98.6%; Pred. No. 7e-73; 1: Indels 1: Ve 2; Mismatches 1; Indels
 Length 450;
 25.6%; Score 268; DB 2; Length 45 ilarity 31.9%; Pred. No. 7.3e-13; Conservative 43; Mismatches 90; Indels
 Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases. EMBL, BC082537; AAH82537.1; -. NON TER 1 1 SEQUENCE 413 AA; 45665 MW; B6EFCA2D6D2CA3C1 CRC64;
 A22FF822CC3CB226 CRC64;
 Last sequence update)
Last annotation update)
 Z
 450
 LYSCMVENPISQGRSLPVKITVYRRSS 207
 Created)
 PRT;
 PROSITE; PS50835; IG LIKE; 2.
SEQUENCE 450 AA; 50114 MW;
 Query Match
Best Local Similarity 98.55
Them 204; Conservative
 (TrEMBLrel. 2 (TrEMBLrel. 2 (TrEMBLrel. 2
 PRELIMINARY;
Director MGC Project;
 Homo sapiens (Human)
 Local Similarity
es 67; Conserv
 ORFNames=UNQ305;
 05-JUL-2004
 Godowski P.;
 05-JUL-2004
05-JUL-2004
 61
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 181
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 Query Match
 WLKV305.
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POVLV-ASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITR 173
 96 DTF-TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPL 154
 95
 40 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITD
 Gaps
 SEQUENCE FROM N.A.
STRAIN=CD-1; TISSUE=Colon;
STRAIN=CD-1; TISSUE=Colon;
MEDLINE=91093141; PubMed=1985902;
Turbide C., Rojas M., Stanners C.P., Beauchemin N.;
"A mouse carcinoembryonic antigen gene family member is a calcium—dependent cell adhesion molecule.";
J. Biol. Chem. 266:309-315(1991).
EMBL; X53084; CAA37251.1; -.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBL_TaxID=10090;
 6
 Query Match
19.4%; Score 202.5; DB 2; Length 278;
Best Local Similarity 32.1%; Pred. No. 5.9e-08;
Matches 54; Conservative 31; Mismatches 74; Indels 9;
 155 LNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITV 202
 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Carcinoembryonic antigen family member protein precursor.
 Potential.
Potential.
1A9CEBF18770258C CRC64;
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EMBL; AY358084; AAQ88451.1;
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 48
 Query Match
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 96 DTF-TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPL 154
 40 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITD 95
 MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment. Genome Res. 13:2265-2270(2003).
 Gaps
 STRAIN=CD1; TISSUE=Colon;
MEDLINE=93273228; PubMed=8500759; DOI=10.1016/0378-1119(93)90716-G;
 McCuaig K., Rosenberg M., Turbide C., Beauchemin N., Nedellec P.,
"Expression of the Bgp gene and characterization of mouse colon
biliary glycoprotein isoforms.";
Gene 127:173-183 (1993).
EMBL, X67283, CAA47700.1; -.
PIR, JC1512, JC1512.
MGD, MGI:1347245; Ceacaml.
InterPro; IPR007110; Ig-like.
 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
 6
 19.4%; Score 202.5; DB 2; Length 341; 32.1%; Pred. No. 7.6e-08; tive 31; Mismatches 74; Indels 9;
 155 LNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITV 202
 341 AA; 36901 MW; B5278D6606996341 CRC64;
 Last sequence update)
Last annotation update)
 292 AA
 Potential
 Created)
 Biliary glycoprotein precursor
 Pfam; PF00047; ig; 1.
SMART; SM00408; IGc2; 1.
PROSITE; PS50835; IG_LIKE; 1.
 Name=Ceacaml; Synonyms=Bgph;
Mus musculus (Mouse).
 us-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, CEACAM3.
 05-JUL-2004 (TrEMBLrel. 27,
 Local Similarity 32.1%
hes 54; Conservative
 PRELIMINARY;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 ORFNames=UNQ3098;
 NCBI_TaxID=9606;
 SEQUENCE
 Query Match
 Signal.
 Q6UY47;
 Q6UY47
 RESULT 8
 Q6UY47
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9
 GENVHLSVVYLPEN----LYSYGWYKGKTVEPNQLIAAYVIDTHVRTPGPAYSGRETISP 103
 131 FTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPI 190
 162 VVLTC-HTMNTGTSPQWIFNNQRLQVTKRMKLSWFNHVLTIDPIRQEDAGEYQCEVSNPV 220
 48 GENVHLSVVYLPEN----LYSYGWYKGKTVEPNQLIAAYVIDTHVRTPGPAYSGRETISP 103
 GKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGT-LR---PDYRDRIRLFE 70
 Succession A.W., Skowronski E., Adamson A.W.,
A Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
A bhan H., Velasco N., Do L., Regala W., Terry A., Carnes J.,
Danganan L., Poundstone P. Christensen M., Georgescu A., Avila J.,
Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
A Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
A Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
A Kobayashi A., Olsen A.S., Carrano A.V.;
Lu Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
RMBL; AG01553; 1LGZ.
RNSSP, QG1553; 1LGZ.
RICHERPO; IPR007110; Ig-like.
RR InterPro; IPR007110; Ig-like.
 15 GKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGT-LR---PDYRDRIRLPE
 71 NGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLELSEA
 11; Gaps
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 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 11;
 Length 235;
 Length 292;
 Indels
 Indels
InterPro; IPR03599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
SMART; SM00409; IG; 2.
SMART; SM00409; IGc, 1.
SMART; SM00409; IGC2, 1.
SMART; SM00409; IGC2, 1.
SMOSTTE; PSS0935; IGC2, 1.
SEQUENCE 292 AA; 32315 MW; 2D4DE785IE301C57 CRC64;
 Last sequence update)
Last annotation update)
 Query Match 17.8%; Score 185.5; DB 2; Best Local Similarity 30.7%; Pred. No. 1.1e-06; Matches 59; Conservative 34; Mismatches 88;
 DB 2;
 18.1%; Score 189.5; DB 2
31.2%; Pred. No. 6.7e-07;
tive 33; Mismatches 88
 235 AA
 Created)
 PRT;
 01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-OCT-2003 (TrEMBLrel. 25,
 Local Similarity 31.2% nes 60; Conservative
 191 SQGRSLPVKITV 202
 221 SSNRSDPLKLTV 232
 PRELIMINARY;
 Homo sapiens (Human)
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 PRT;
 1 34 P
521 AA, 56630 MW,
 PROSITE; PS50835; IG LIKE; 3
 1 Similarity 27.8% 47; Conservative
 PRELIMINARY;
 Pfam; PF00047; ig; 3. SMART; SM00408; IGc2; 3.
 Mus musculus (Mouse)
 sequence. (Fragment)
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI TaxID=10090;
 SEQUENCE
 Name=Ly9;
 Query Match
Best Local S
Matches 47
 SIGNAL
 Q8C9E4
 Signal
 RESULT 12
Q8C9E4
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 131 FTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPI 190
 DTF-TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNC-SHENGTKPSYTWLKDGKP 153
 ENFRRIEATVQFHVHQLLLKPNITSNNSNPVEGDDSVSLTCDSYTDPDNITYLWSRNGES 186
 162 VVLTC-HTNNTGTSFQWIFNNORLOVTKRMKLSWFNHMLTIDPIROEDAGEYOCEVSNPV
SGDLHFQNVTLEDTGYYTLQVTYRNSQIE-QASHHLRVYBSVAQPSIQASSTTVTE-KGS
 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITD
 Gaps
 01-NOV-1996 (TERMELTEI. 01, Last sequence update)
01-OCT-2003 (TERMELTEI. 25, Last annotation update)
Biliary glycoprotein precursor.
Bame-Ceacani, Synonyms-Bgpe;
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Musin
 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Biliary glycoprotein precursor.
Name=Ceaccaml; Synonyms=Bgpf;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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6
 154 LLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITV 202
 Length 458;
 80; Indels
 49671 MW; 1DC61FFCD875B85F CRC64;
 17.3%; Score 181; DB 2; 27.8%; Pred. No. 5.3e-06;
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 34; Mismatches
 458
 521
 Potential
 (TrEMBLrel. 01, Created)
 Created)
 PRT;
 PRT;
 Pfam; PF00047; 1g; 3.
SMART; SM00408; IGc2; 3.
PROSITE; PS50835; IG_LIKE; 3.
 (TrEMBLrel. 01,
 SQGRSLPVKITV 202
 SSNRSDPLKLTV 232
 Conservative
 PRELIMINARY;
 PRELIMINARY;
 458 AA;
 Local Similarity
tes 47; Conserv
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 061352;
01-NOV-1996 (
01-NOV-1996 (
 01-NOV-1996
 221
 SEQUENCE
 40
 96
 127
 187
 191
 Query Match
 Signal.
SIGNAL
 RESULT 10
061351
1D 061355
AC 061335
AC 061335
AC 061335
DT 01-NO
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 Matches
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Q61352 ID Q6 Q6 DT Q1 DT 01 DT 01 DE Bi GN Na OC Ev

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96 DIF-IGEKTINLIVDVPISRPQVLVASTIVLELSEAFTLNC-SHENGTKPSYTWLKDGKP 153
 40 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITD
 [1] -
SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Thymus;
MEDLINE-99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
 Gaps
 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630078M16 product:lymphocyte antigen 9, full insert
SEQUENCE FROM N.A.
STRAIN=CDI, TISSUE-COLON;
STRAIN=CDI, TISSUE-COLON;
MEDLINE-93273228; PubMed-8500759; DOI=10.1016/0378-1119(93)90716-G;
MCCuaig K., Rosenberg M., Turbide C., Beauchemin N., Nedellec P.;
"Expression of the Bgp gene and characterization of mouse colon dene 127:173-183(1993)."
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
 RIKEN FANTOM Consortium;
"Functional annotation of a full-length mouse cDNA collection.";
 8;
 154 LLNDSRMLLSPDQKVLTITRVLMBDDDLYSCMVENPISQGRSLPVKITV 202
 Length 521;
 LSEGDRIKLSEGNRTLTILLNVTRNDTGPYVCETRNPVSVNRSDPFSLNI
 80; Indels
 STRAIN=CD1; TISSUE=COlon;

Huang D.C., Huang X.F., Novel M., Novel G.;

Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.

EMBL; X67281; CAA47698.1; -.

PIR; S34338; S34338.

HSSP; Q61353; IL6Z.

HGDP, MGI:1347245; Ceacaml.

InterPro; IPR007100; IG-1ike.
 STRAIN=C57BL/6J; TISSUB=Thymus;
MEDLINE=21085660; Pubmed=11217851; DOI=10.1038/35055500;
 Potential.
566DFEB9F2F87FCD CRC64;
 17.3%; Score 181; DB 2; 27.8%; Pred. No. 6.2e-06; ive 34; Mismatches 80
 538 AA.
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219 PYTCKAWNPVSQNSSQPVRI 238
 Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 2.
PROSITE; PS50835; IG LIKE; 2.
NON_TER
 181 LYSCMVENPISQGRSLPVKI
 cDNA sequences."
 PRELIMINARY;
 Ly9 protein (Fragment)
 Mus musculus (Mouse)
 SEQUENCE FROM N.A.
 FROM N.A.
 NCBI TaxID=10090;
 05-JUL-2004
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 50 TPPTVISGMLGGSVTFSLNISKDAEIEHII-WNC---PPKALALVFYKKDITTLDKGYNG 105
 65 RIRLFENG-SLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVASTT 123
 124 VLEL-SEAFTLNCSHENGTKPS--YTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TO STUDE-Thymus;

MEDLINE=C57BL/6J; TISSUE=Thymus;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Hazada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M.,

Noneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

genome Res. 10:1757-1771(2000).
 the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
 SECUENCE FROM N.A.
SETRALN=C57BL/6J; TISSUB=Thymus;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Mornalization and subbraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
 17.3%; Score 180.5; DB 2; Length 538; 27.5%; Pred. No. 7.1e-06;
 90; Indels
 538 AA; 60040 MW; 7DC7FB9C64BFE9A6 CRC64;
 40; Mismatches
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The FANTOM Consortium,
 PROSITE; PS50835; IG_LIKE; 2.
NON_TER 538 538
 Conservative
 Nature 409:685-690(2001)
 Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 2.
 Local Similarity
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SUCHANGE FROW N.A.

SECURATION OF TISSUE-Hematopoietic Stem Cell;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; Medline G.D.,

MEDLINE=22460399;

MEDLINE=22388257; PubMed=127, Medline M.K.,

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MEDLINE=22460399;

MEDLINE=2246039;

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 96
 64
 41 TPPTVISGMLGGSVTFSLNISKDAEIEHII-WNC---PPKALALVFYKKDITILDKGYNG
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 DB 2; Length 645;
 Indels
 Strausberg R ;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases
 645 AA; 71884 MW; 316EF183DFD510BB CRC64;
 (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
 STRAIN-C57BL/6NCr; TISSUE-Hematopoietic Stem Cell;
 / Match 17.3%; Score 180.5; DB 2; Local Similarity 27.5%; Pred. No. 8.8e-06; Les 55; Conservative 40; Mismatches 90;
 645 AA.
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NCBI_TaxID=10090;
 AF246700;
 AF245117;
 AF245506;
 AF245508;
 AF245118;
 AF245510;
 AF246699
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 Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler Caralbidens, Proposition of the control of the
124 VLEL-SEAFTLNCSHENGTKPS--YTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 RIRLPENG-SLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVASTT 123
 5 SPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRD 64
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 17.3%; Score 180.5; DB 2; Length 649; 27.5%; Pred. No. 8.9e-06; ive 40; Mismatches 90; Indels 15;
 Strausberg R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO55380; AAH55380.1; --
HSSP; P08921; 1HNG.
 649 AA; 72414 MW; AD6A09381C063B34 CRC64;
 Last sequence update)
Last annotation update)
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 SEQUENCE FROM N.A. STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
 649 AA
 GO; GO:0005615; C:extracellular space; TAS. GO; GO:0016021; C:integral to membrane; TAS
 Created)
 PRT;
 181 LYSCMVENPISQGRSLPVKI 200
 210 PYTCKAWNPVSQNSSQPVRI 229
 Pfam, PF00047; ig; 1. SMART; SM00409; IG; 2. PROSITE; PS50835; IG_LIKE; 2.
 InterPro, IPR003599; Ig.
InterPro, IPR007110; Ig-like.
 (TrEMBLrel. 25, (TrEMBLrel. 25, (TrEMBLrel. 26,
 Local Similaricy -
 CDNA sequences.
 PRELIMINARY;
 protein (Fragment).
 Mus musculus (Mouse).
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
101 RLKVSEDGYSLYMSNLTKSDSGSYHAQINQKNVILTTNKEFTLHIYEKLQKPQIIVESVT 160
 124 VLEL-SEAFTINCSHENGTKPS--YTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 180
 -----DIHLNIYDGSHTLRVSQSVCDPDL 213
 SEQUENCE FROM N.A., AND POLYMORPHISM.
STRAIN=129/Sv, BALB/c, and C57BL/6; TISSUE-Spleen;
MEDLINE=20424510; PubMed=10970093; DOI=10.1107/s002510000209;
TOVAR V., de la Fuente M.A., Pizcueta P., Bosch J., Engel P.;
"Gene structure of the mouse leukocyte cell surface molecule Ly9.";
 LY9 MOUSE STANDARD; PRT; 654 AA.

Q01965; Q9ES29; Q9ES35; Q9ES36;
01-UIN-1994 (Rel. 29, Created)
8-FEB-2003 (Rel. 41, Last sequence update)
05-UIN-2004 (Rel. 44, Last annotation update)
T-lymphocyte surface antigen Ly-9 precursor (Lymphocyte antigen 9)
 MEDLINE=92373005; PubMed=1506686;
Sandrin M.S., Gumley T.P., Henning M.M., Vaughan H.A., Gonez L.J.,
Trapani J.A., McKenzie I.F.C.;
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
 SEQUENCE OF 22-654 FROM N.A., AND SEQUENCE OF 48-59.
 or send an email to license@isb-sib.ch).
 AAG13268.2; JOINED
 214 PYTCKAWNPVSQNSSQPVRI 233
 [mmunogenetics 51:788-793(2000).
 EMBL; AF244131; AAG14997.1; -.
 181 LYSCMVENPISOGRSLPVKI
 MGD; MGI:96885; Ly9.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
 AF244130; AAG14996.1;
 AF246701; AAG13268.2;
 AAG13268.2;
 AAG13268.2;
AAG13268.2;
 AAG13268.2;
 AAG13268.2;
AAG13268.2;
 AAG13268.2;
 MBL; M84412; AAA39468.1;
 Name=Ly9; Synonyms=Ly-9; Mus musculus (Mouse).
 Pfam; PF00047; ig; 2.
SMART; SM00409; IG; 2
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50 TPPTVISGMLGGSVTFSLNISKDAEIEHII-WNC---PPKALALVFYKKDITILDKGYNG 105
 65 RIRLFENG-SILLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVASTT 123
 124 VLEL-SEAFTINCSHENGTKPS--YTWLKDGKPLINDSRMLLSPDQKVLTITRVLMEDDD 180
 64
PROSITE, PS50835; IG LIKE; 2.

W Antigen; Cell adhesion; Direct protein sequencing; Glycoprotein; Immunoglobulin domain; Polymorphism; Repeat; Signal; Transmembrane.

SIGNAL

TRANSMEM

48 654 T-lymphocyte surface antigen Ly-9.

DOMAIN

48 654 F-lymphocyte surface antigen Ly-9.

TRANSMEM

454 474 Cytoplamic (Potential).

TRANSMEM

455 654 Cytoplamic (Potential).

TRANSMEM

456 147 Cytoplamic (Potential).

TOMAIN

159 243 Ig-like C2-type 1.

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250 362 Ig-like V-type 2.

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159 242 Potential.

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 5 SPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRD
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17.3%; Score 180.5; DB 1; Length 654;
Best Local Similarity 27.5%; Pred. No. 9e-06;
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E -> K (in Ly9-1).
A -> I (in Ly9-1).
G -> E (in Ly9-1).
F -> L (in Ref. 2).
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 181 LYSCMVENPISQGRSLPVKI 200
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219 PYTCKAWNPVSQNSSQPVRI 238
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1 MKRERGALSRASRALRLAPF......TAGVHIIREQDEAGPVEISA 416
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 2105692 seqs, 386760381 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:*
 A_Geneseq_16Dec04:*
 geneseqp1980s:*
geneseqp1990s:*
 geneseqp2000s:*
 seq length: 0
seq length: 200000000
 US-10-706-691-16
 Perfect score:
Sequence:
 Scoring table:
 Minimum DB 8
Maximum DB 8
 Database :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|            | ion             | Predicted | Human INS | Human pro | Human the | Murine IN | Human mat | Novel hum |          | Human pro | Human the | INSP052 e | Human mat | Human pro |          | Human EST | Human the | Human the | Human tra | Human INS | Human INS | Human INS | Human pro | Amino aci |          |          |
|------------|-----------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|----------|-----------|-----------|-----------|-----------|-----------|----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|----------|----------|
|            | Description     | Abg75379  | Abg75377  | Ado47892  | Ads11056  | Abg75378  | Ado47895  | Adq65357  | Aae14784 | Ado47887  | Ads11055  | Abg75380  | Ado47890  | Adm87341  | Aam24238 | Adm87787  | Ads12269  | Ads12268  | Aae26421  | Abg75371  | Abg75376  | Abg75372  | Aam78339  | Aay13398  | Adc78632 | Aab80266 |
|            |                 |           |           |           |           |           |           |           |          |           |           |           |           |           |          |           |           |           |           |           |           |           |           |           |          |          |
|            | £               | ABG75379  | ABG75377  | AD047892  | ADS11056  | ABG75378  | ADO47895  | ADQ65357  | AAE14784 | ADO47887  | ADS11055  | ABG75380  | ADO47890  | ADM87341  | AAM24238 | ADM87787  | ADS12269  | ADS12268  | AAE26421  | ABG75371  | ABG75376  | ABG75372  | AAM78339  | AAY13398  | ADC78632 | AAB80266 |
|            | 82              | 7         | 7         | 8         | œ         | 7         | æ         | œ         | 'n       | œ         | ω         | 7         | æ         | œ         | 4        | œ         | æ         | œ         | ა         | 7         | 7         | 7         | 4         | ~         | m        | 4        |
|            | Match Length DB | 416       | 416       | 416       | 416       | 418       | 383       | 367       | 298      | 270       | 270       | 246       | 237       | 256       | 256      | 256       | 256       | 256       | 224       | 114       | 100       | 188       | 338       | 450       | 450      | 450      |
| *<br>Query | Match           | 100.0     | 100.0     | 100.0     | 100.0     | 93.9      | 92.5      | 69.7      | 69.4     | 63.7      | 63.7      | 56.8      | 56.2      | 56.0      | 55.5     | 55.5      | 55.5      | 55.5      | 54.5      | 26.9      | 24.6      | 22.8      | 13.3      | 13.3      | 13.3     | 13.3     |
|            | Score           | 2122      | 2122      | 2122      | 2122      | 1992      | 1962      | 1478.5    | 1472     | 1352      | 1352      | 1205      | 1192      | 1189      | 1178     | 1178      | 1178      | 1178      | 1157      | 570       | 522       | 484       | 282       | 282       | 282      | 282      |
| Result     | No.             | г         | 8         | m         | 4         | ហ         | 9         | 7         | σ0       | σ         | 10        | 11        | 12        | 13        | 14       | 15        | 16        | 17        | 18        | 19        | 50        | 21        | 22        | 23        | 24       | 25       |

The present invention provides the protein and coding sequences of a novel human immunoglobulin domain-containing cell surface recognition molecule known as INSP05. The polypeptide is useful as immunoglobulin domain-containing cell surface recognition molecule. The sequences may also be used in therapy or diagnosing a disease or in the manufacture of a medicament for treating a disease. The disease is a cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, psychiatric, developmental, genetic or metabolic disorder, an infection or other pathological condition. The polypeptides and nucleic acids are essential to the structural integrity and homeostatic functioning of most tissues.

| Aau12360 Human PRO | Aau81958 Human PRO | Abu71644 Human PRO | Abol7804 Novel hum | Abu71499 Human PRO | Abu81058 Human PRO | Abu71945 Human sec | Novel | Abu66758 Human PRO | Abu54401 Human sec | Abo47416 Human sec | Novel        | Abo25029 Human sec | Abu64553 Human sec | Abu67399 Human sec | Abol4919 Human sec | Abu67034 Human sec | Abu69676 Novel hum | Abol4858 Human sec | Ada45897 Novel hum |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------|--------------------|--------------------|--------------------|--------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| 4 AAU12360         | ) 5 AAU81958       | ) 6 ABU71644       | ) 6 ABO17804       | 6 ABU71499         | ) 6 ABU81058       | 6 ABU71945         | 9     | ) 6 ABU66758       | 9                  | 6                  | 0 6 ABU59839 | 9                  | 6 ABU64553         | 6 ABU67399         | 6 ABO14919         | 6 ABU67034         | 6 ABU69676         | 6 ABO14858         | 6 ADA45897         |
| 32 13.3 450        |                    | 13.3               |                    | 13.3               | 13.3               | 13.3               | 13.3  | 13.3               | 13.3               | 13.3               | 13.3         | 13.3               | 32 13.3 450        | 13.3               | 13.3               |                    |                    | 13.3               |                    |
| 26 28              | 27 28              | 28 28              | 29 . 28            | 30 26              | 31 26              | 32 28              | 33 28 | 34 28              | 35 28              | 36 28              | 37 28        | 38 28              | 39 282             | 40 28              | 41 28              | 42 28              | 43 28              | 44 28              | 45 28              |

## ALIGNMENTS

New INSP052 polypeptides and nucleic acids, useful in diagnosing and treating cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, psychiatric, developmental, genetic or metabolic disorder. INSP052; human; cell proliferation; autoimmune disease; inflammation; cardiovascular disease; neurological disease; psychiatric disease; developmental disease; metabolic disorder; infection; infection; immunoglobulin domain-containing cell surface recognition molecule. ΰ Power ABG75379 standard; protein; 416 AA Phelps CB, Example 2; Fig 5; Opp; English. 30-APR-2003; 2003WO-GB001851. 30-APR-2002; 2002GB-00009884. Predicted INSP052 protein. (first entry) (ARES-) ARES TRADING SA. Fagan RJ, WPI; 2003-903655/82. N-PSDB; ACH01277. WO2003093316-A2 Unidentified. 13-NOV-2003. 22-APR-2004 Davids AR, ABG75379; RESULT 1 ABG75379 

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Claim 1; Page 67; Opp; English.
 Sequence 416 AA;
 WO2004007672-A2
 Homo sapiens
 L5-JUL-2004
 22-JAN-2004
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 121
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 ADO47892;
 RESULT
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 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY 120
 180
 EVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVJELSEAFTLNCSHENGTKPSYTW 180
 240
 LKDGKPLINDSRMLLSPDQKVLTITRVLMEDDDLYSCRVENPISQGRSLPVKITVYRRSS 240
 LYIILSTGGIFLLVTLVTVCACWKPSKRKQKKLEKQNSLEYMDQNDDRLKPEADTLPRSG 300
 LYIILSTGGIFLLVTLVTVCACWKPSKRKQKKLEKQNSLEYMDQNDDRLKPEADTLPRSG 300
 EQERKNPMALYILKDKDSPETEENPAPEPRSATEPGPPGYSVSPAVPGRSPGLPIRSARR 360
 9
 New INSP052 polypeptides and nucleic acids, useful in diagnosing and treating cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, psychiatric, developmental, genetic or metabolic disorder.
 EQERKNPMALYILKDKDSPETEENPAPEPRSATEPGPPGYSVSPAVPGRSPGLPIRSARR
 MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST
 EVEISITDDTFTGEKTINLTVDVPISRPOVLVASTTVLELSEAFTLNCSHENGTKPSYTW
 LKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSS
 361 YPRSPARSPATGRTHSSPPRAPSSPGRSRSASRTLRTAGVHIIREQDEAGPVEISA 416
 1 MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST
 361 YPRSPARSPATGRIHSSPPRAPSSPGRSRSASRTLRTAGVHIIREQDEAGPVEISA 416
 INSP052; human; cell proliferation; autoimmune disease; inflammation; cardiovascular disease; neurological disease; psychiatric disease; developmental disease; metabolic disorder; infection; metabolic disorder; infection; metaboluc developmental disease; metabolic disorder; infection;
 Gaps
 ö
 Length 416;
 a polypeptide shown in the invention
 Indels
 100.0%; Score 2122; DB 7;
100.0%; Pred. No. 2.4e-146;
ive 0; Mismatches 0;
 ΰ
 Power
 e)
 ABG75377 standard; protein; 416
 Human INSP052 complete protein.
 Phelps
 30-APR-2003; 2003WO-GB001851
 30-APR-2002; 2002GB-00009884
 (first entry)
 Conservative
 The present sequence is
 SA
 Davids AR, Fagan RJ,
 (ARES-) ARES TRADING
 WPI; 2003-903655/82.
 Local Similarity
nes 416; Conserv
 N-PSDB; ACH01275
 Š
 WO2003093316-A2.
 Sequence 416
 Homo sapiens
 22-APR-2004
 13-NOV-2003
 121
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 301
 61
 61
 121
 181
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 241
 Query Match
 ABG75377
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 ABG75377
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 human; virucide; anti-HIV; cytostatic; antinflammatory; antiallergic; fimunosuppressive; antiatreriosclerotic; hypotensive; osteopathic; antianemic; neuroprotective; nootropic; antiparkinsonian; antiathmatic; haemostatic; antidiabetic; cardiant; HIV; viral infection; cancer; inflammation; allergy; graft rejection; atherosclerosis; hypertension; osteoporosis; anaemia; Alzheimer's disease; Parkinson's disease; asthma; diabetes; myocardial infarction; haemophilia.
 120
 120
 180
 180
 240
 240
 300
 360
 301 EQERKNPMALYILKDKDSPETEENPAPEPRSATEPGPPGYSVSPAVPGRSPGLPIRSARR 360
 novel human immunoglobulin domain-containing cell surface recognition molecule known as INSP052. The polypeptide is useful as immunoglobulin domain-containing cell surface recognition molecule. The sequences may also be used in therapy or diagnosing a disease or in the manufacture of a medicament for treating a disease. The disease is a cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, psychiatric, developmental, genetic or metabolic disorder, an infection or other pathological condition. The polypeptides and nucleic acids are essential to the structural integrity and homeostatic functioning of most tissues. The present sequence is a polypeptide shown in the invention
 9
 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY
 LYIILSTGGIFLLVTLVTVCACWKPSKRKQKKLEKQNSLEYMDQNDDRLKPEADTLPRSG
 1 MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST
 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY
 EVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTW
 LKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSS
 EQERKNIPMALYILKDKDSPETEENPAPEPRSATEPGPPGYSVSPAVPGRSPGLPIRSARR
 YPRSPARSPATGRIHSSPPRAPSSPGRSRSASRILRIAGVHIIREQDEAGPVEISA 416
 YPRSPARSPATGTHSSPPRAPSSPGRSRSASRTLRTAGVHIIREQDEAGPVEISA 416
The present invention provides the protein and coding sequences of novel human immunoglobulin domain-recritical
 ö
 Length 416;
 Indels
 Query Match 100.0%; Score 2122; DB 7; Best Local Similarity 100.0%; Pred. No. 2.4e-146; Matches 416; Conservative 0; Mismatches 0;
 ADO47892 standard; protein;
 Human protein SEQ ID NO:9.
 (first entry)
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 5
 The invention relates to novel isolated polymucleotides and polypeptides encoded by them. Also included are mutants or variants of the proceed by them. Also included are mutants or variants of the polypeptides. A polypeptide of the invention has virucide, anti-HIV, cytostatic, antidiplammatory, antiallergic, immunosuppressive, antialtergic, antidiabetic, and cardiant activity. The composition antiasthmatic, haemostatic, antidiabetic, and cardiant activity. The composition and methods are useful in diagnostics, forensics, gene or chromosome mapping, identification of mutations responsible for genetic disorders or other traits, in assessing biodiversity, or in producing many other types of data and products dependent on DNA and amino acid sequences. They may also be used in preventing or treating diseases (e.g. HIV and other viral infections, cancer, inflammation, allergies, graft rejection, attentions answering, Alzheimer's disease, asthma, diabetes, myocardial infarction or haemophilia). They may also be used as targets in drug screening. The present sequence represents a polypeptide of the invention.
 New isolated polypeptides and polynucleotides useful in diagnostics, forensics, in preventing or treating diseases such as HIV and cancer, and
 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY 120
 LKDGKPLINDSRMLLSPDGKVLTITRVLMEDDDLYSCRVENPISGGRSLPVKITVYRRSS 240
 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY 120
 EVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTW 180
 LKDGKPLINDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSS 240
 LYIILSTGGIFLLVTLVTVCACWKPSKRRQKKLEKQNSLEYMDQNDDRLKPEADTLPRSG 300
 EQERKNPMALYILKDKDSPETEENPAPEPRSATEPGPPGYSVSPAVPGRSPGLPIRSARR 360
 1 MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST 60
 1 MKRERGALSRASRALRLAPPVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST
 YPRSPARSPARGETHSSPPRAPSSPGRSRSASRTLRTAGVHITREQDEAGPVEISA 416
 Gaps
 ö
 100.0%; Score 2122; DB 8; Length 416; 100.0%; Pred. No. 2.4e-146; ive 0; Mismatches 0; Indels 0
 Ľ,
 Wang ZW,
 Claim 10; SEQ ID NO 9; 205pp; English.
 Wehrman T,
09-JUL-2003; 2003WO-US021703.
 2002US-0395402P
 Д,
 Conservative
 Zhou
 WPI; 2004-122914/12.
N-PSDB; ADO47891.
 (NUVE-) NUVELO INC
 Similarity
 Rupp F, Wang J,
 AA;
 drug targets.
 12-JUL-2002;
 Sequence 416
 416;
 241
 121
 361
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 181
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 Query Match
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ADS11056 standard; protein; 416 AA

RESULT 4 ADS11056 ID ADS1

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The invention relates to a novel isolated polynucleotide and the encoded polypeptide. The molecules of the invention demonstrate antinflammatory, neuroprotective, antianaemic, cytostatic and vulnerary activities and may be useful in preparing a composition for diagnosing or treating inflammatory, haematopoleiti, immune, neurodegenerative or stem cell disorders, such as aplastic anaemia or cancer, as well as for promoting wound healing. The molecules may also be utilised during gene therapy procedures. The current sequence is that of a human therapeutic protein of the invention. The current sequence is not shown explicitly within the specification but can be accessed from the WIPO web-site.
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 240
 120
 120
 180
 240
 LYIILSTGGIFLLVTLVTVCACWKPSKRKQKKLEKQNSLEYMDQNDDRLKPEADTLPRSG 300
 301 EQERKNPMALYILKDKDSPETEENPAPEPRSATEPGPPGYSVSPAVPGRSPGLPIRSARR 360
 9
 9
 Zhou P;
 ö
 antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary; inflammatory; haematopolesis; immunity; neurodegenerative; stem cell; aplastic anaemia; cancer; wound healing; gene therapy.
 181 LKDGKPLINDSRMILSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSS
 1 MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST
 EVEISITDDTFTGEKTINLTVDVPISRPOVLVASTTVLELSEAFTLNCSHENGTKPSYTW
 1 MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST
 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY
 61 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY
 LKDGKPLLNDSRMLLSPDQKVLTITRVLMBDDDLYSCMVENPISQGRSLPVKITVYRRSS
 New polynucleotide, useful in preparing a composition for diagnosing treating inflammatory, neurodegenerative or stem cell disorders, e.g. aplastic anemia or cancer for promoting wound healing.
 Gaps
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y G, Z
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Weng
 Length 416;
 Indels
 Wang
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Xue
 100.0%; Score 2122; DB 8;
100.0%; Pred. No. 2.4e-146;
live 0; Mismatches 0;
 Wehrman
 Asundi V, Ren F, Zhang J, Wehrman
Chen R, Zhao QA, Wang J, Ghosh M,
 Claim 20; SEQ ID NO 1293; 718pp; English.
 Human therapeutic protein - SEQ ID 1293.
 30-SEP-2003; 2003WO-US030720.
 02-OCT-2002; 2002US-0416186P
 Best Local Similarity 100.
Matches 416; Conservative
 WPI; 2004-668857/65.
N-PSDB; ADS10372.
 (NUVE-) NUVELO INC
 Sequence 416 AA;
 #O2004080148-A2
 Homo sapiens
 23-SEP-2004
 YT,
ADS11056;
 61
 121
 181
 241
 Query Match
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The invention relates to novel isolated polynucleotides and polypeptides encoded by them. Also included are mutants or variants of the polynucleotides and polypeptides. A polypeptide of the invention has virucide, anti-HIV, cytostatic, antiinflammatory, antiallergic, immunosuppressive, antiarteriosclerotic, hypotensive, osteopathic, haemostatic, autiorprotective, noctropic, antiparkinsonian, antiasthmatic, haemostatic, antidiabetic, and cardiant activity. The composition and methods are useful in diagnostics, forensics, gene or chromosome mapping, identification of mutations responsible for genetic disorders or other traits, in assessing biodiversity, or in producing many other types of data and products dependent on DNA and amino acid sequences. They may also be used in preventing or treating diseases (e.g. HIV and other viral
 immunosuppressive, antiarteriosclerotic; hypotensive; osteopathic; antianaemic; neuroprotective; nootropic; antiparkinsonian; antiasthmatic; haemostatic; attidiabetic; cardiant; HIV; viral infection; cancer; inflammation; allergy; graft rejection; atherosclerosis; hypertension; osteoporosis; anaemia; Alzheimer's disease; Parkinson's disease; asthma; diabetes; myocardial infarction; haemophilia.
 New isolated polypeptides and polynucleotides useful in diagnostics, forensics, in preventing or treating diseases such as HIV and cancer, and
241 LYIILSTGGIFLLVTLVTVCACWKPSKKSRKKRKLEKQNSLEYMDQNDDRLKSEADTLPR 300
 301 SGEQERKNPWALYILKDKDSSEPDENPATEPRSTTEPGPPGYSVSPPVPGRSPGLPIRSA 360
 SGEQERKNPMALYILKUKUSPETEENPAPEPRSATEPGPPGYSVSPAVPGRSPGLPIRSA 358
 RRYPRSPARSPATGRIHSSPPRAPSSPGRSRSASRILRTAGVHIIREQDEAGPVEISA 416
 human; virucide; anti-HIV; cytostatic; antiinflammatory; antiallergic;
 LKDGKPLINDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSS
 181 LKDGKPLINDSRMILSPDQKVLTITRVLMEDDDLYSCVVENPISQVRSLPVKITVYRRSS
 LYIILSTGGIFLLVTVTVCACWKPSK--RKQKKLEKQNSLEYMDQNDDRLKPEADTLPR
 RRYPRSPARSPATGRIHITSPPRAPSSPGRSRSSRSLRTAGVQRIREQDESGQVEISA
 YT;
 Tang
 Wang ZW,
 Claim 10; SEQ ID NO 12; 205pp; English.
 Wehrman T,
 Ä
 Human mature protein SEQ ID NO:12.
 ADO47895 standard; protein; 383
 09-JUL-2003; 2003WO-US021703.
 12-JUL-2002; 2002US-0395402P.
 Rupp F, Wang J, Zhou P,
 (first entry)
 WPI; 2004-122914/12.
N-PSDB; ADO47893.
 (NUVE-) NUVELO INC.
 WO2004007672-A2.
 drug targets.
 Homo sapiens.
 15-JUL-2004
 22-JAN-2004
 241
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 ADO47895;
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 novel human immunoglobulin domain-containing cell surface recognition molecule known as INSP052. The polypeptide is useful as immunoglobulin domain-containing cell surface recognition molecule. The sequences may also be used in therapy or diagnosing a disease or in the manufacture of a medicament for treating a disease. The disease is a cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, psychiatric, developmental, genetic or metabolic disorder, an infection or other pathological condition. The polypeptides and nucleic acids are essential to the structural integrity and homeostatic functioning of most tissues. The present sequence is a polypeptide shown in the invention
 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY 120
 121 EVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTW 180
 1 MKRERGALSRASRALRLSPFVYLLLIQPVPLEGVNITSPVRLIHGTVGKSALLSVQYSST 60
 New INSP052 polypeptides and nucleic acids, useful in diagnosing and treating cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, psychiatric, developmental, genetic or metabolic disorder.
 1 MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST
 INSP052; human; cell proliferation; autoimmune disease; inflammation; cardiovascular disease; neurological disease; psychiatric disease; developmental disease; metabolic disorder; infection; amminoglobulin domain-contening cell surface recognition molecule.
 Gaps
 YPRSPARSPATGRTHSSPPRAPSSPGRSRSASRTLRTAGVHIIREQDEAGPVEISA
 361 YPRSPARSPATGRTHSSPPRAPSSPGRSRSASRTLRTAGVHIIREQDEAGPVEISA
 present invention provides the protein and coding sequences
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7
 Length 418;
 12; Indels
 93.9%; Score 1992; DB 7;
94.3%; Pred. No. 7.4e-137;
ive 10; Mismatches 12;
 ΰ
 Power
 ABG75378 standard; protein; 418 AA
 Phelps CB,
 Example 1; Page 68; Opp; English.
 Murine INSP052 complete protein.
 30-APR-2003; 2003WO-GB001851.
 30-APR-2002; 2002GB-00009884.
 (first entry)
 Conservative
 TRADING SA
 Davids AR, Fagan RJ,
 WPI; 2003-903655/82.
 Similarity
 N-PSDB; ACH01276
 Sequence 418 AA;
 WO2003093316-A2.
 (ARES-) ARES
 22-APR-2004
 13-NOV-2003.
 394;
 361
 Query Match
Best Local S
 61
 ABG75378
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Sequence 367 AA;
 Homo sapiens
 30-OCT-2002
 AAE14784;
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 Peptide
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 DYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 153
 213
 180
 273
 EKQNSLEYMDQNDDRLKPEADTLPRSGEQERKNPMALYILKDKDSPETEENPAPEPRSAT 333
 EPGPPGYSVSPAVPGRSPGLPIRSARRYPRSPARSPATGRTHSSPPRAPSSPGRSRSASR 393
 osteopathic, neuroprotective, nootropic, antiparkinsonian, cytostatic, gene therapy, diagnostic marker, morbid state, osteoporosis, neurological disease, Alzheimer's disease, Parkinson's disease, dementia,
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 93
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infections, cancer, inflammation, allergies, graft rejection, atherosclerosis, hypertension, osteoporosis, anaemia, Alzheimer's disease, asthma, diabetes, myocardial infarction haemophilial. They may also be used as targets in drug screening. The present sequence represents a polypeptide of the invention.
 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD
 LYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACWKPSKRKQKKL
 34 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 STIVLELSEAPTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD
 LYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACWKPSKRKQKKL
 Gaps
 Ishii S;
 ö
 92.5%; Score 1962; DB 8; Length 383; 100.0%; Pred. No. 1e-134; ive 0; Mismatches 0; Indels
 Ή,
 Sato
 Wakamatsu A,
 Otsuki T, Wakama
Nagai K, Irie R;
 TLRTAGVHIIREQDEAGPVEISA 416
 Z
 Novel human protein sequence #330
 ADQ65357 standard; protein; 367
 (REAS-) RES ASSOC BIOTECHNOLOGY
 2003JP-00102206.
2003JP-00131392.
 21-JAN-2004; 2004EP-00001196
 (first entry)
 al Similarity 100.
383; Conservative
 Sugiyama T,
Isono Y,
 WPI; 2004-535376/52
 Sequence 383
 sapiens.
 EP1440981-A2
 21-JAN-2003;
 09-MAY-2003;
 Yamamoto J,
 07-0CT-2004
 28-JUL-2004
 Isogai T,
 241
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 Query Match
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The invention relates to 2495 novel polynucleotides (I) and their encoded polypeptides, sequences hybridizing to these nucleotides, sequences encoding partial polypeptides and sequences having 70% to 90% identity to the nucleotide and protein sequences. The nucleotides and polypeptides are useful as diagnostic markers or therapeutic target for the diseases or morbid states. They are also useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, sequence of the invention.
 240
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 180
 LYIILSTGGIFLLVTLVTVCACWKPSKRKQKKLEKQNSLEYMDQNDDRLKPEADTLPRSG 300
 301 EQERKNPMALYI------LKDKDSPETEENPAPEPRS-ATEPGPPGYSVSPAVPGR 349
 ::|: | :: | :: | | | | :: | 354
Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
 9
 9
 121 EVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTW
 MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST
 61 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDSRDRIRLFENGSLLLSDLQLADBGTY
 LKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSS
 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY
 1 MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST
 EVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTW
 Gaps
 Human, immunoglobulin superfamily protein-4; IGSFP-4; asthma, immune system disorder; acquired immune deficiency syndrome; AIDS; atheroscleroscis; neurological disorder; Alzheimer's disease; barkinson's disease; developmental disorder; renal tubular acidosis; anaemia; muscle disorder; cardiomyopathy; myocarditis; cancer;
 17;
 Query Match 69.7%; Score 1478.5; DB 8; Length 367; Best Local Similarity 84.7%; Pred. No. 1.9e-99; Matches 305; Conservative 12; Mismatches 26; Indels 17;
 cell proliferative disorder; arteriosclerosis; hepatitis.
 Human immunoglobulin superfamily protein (IGSFP)-4.
 Claim 1; SEQ ID NO 2518; 2449pp; English.
 34. .298
/note= "Mature IGSFP-4"
43. .231
 1. .33
/label= Signal_peptide
 Location/Qualifiers
 Ŕ
 AAE14784 standard; protein; 298
 (first entry)
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The present sequence is human immunoglobulin superfamily protein (IGSFP)-

1. The IGSFP polypeptide and polymucleotide are useful for diagnosing,

2. The IGSFP polypeptide and polymucleotide are useful for diagnosing,

2. Immune system disorders associated with aberrant expression of

2. IGSFP e.g. immune system disorders (e.g. acquired immune deficiency

2. Immune system disorders (e.g. Alzheimer's disease, Huntington's disease,

2. Alzheimer's disease, Huntington's disease,

2. dementa, Parkinson's disease), developmental disorders (e.g. renal

2. tubular acidosis, epilepsy, anaemia), muscle disorders (e.g.

2. cardiomyopathy, myocarditis), or cell proliferative disorders

2. cardiomyopathy, myocarditis, heatilfs, and cancer). The polypeptide and

2. polymucleotide are also useful for assessing the effects of exogenous

3. compounds on their expression. The polypeptide is useful in drug

3. screening techniques, to analyse the proteome of a tissue or call type,

3. selements on a microarray. The polymucleotide is useful for creating

3. knock-in humanised animals or transgenic animals to model human diseases,

3. in somatic or germline gene therapy, to generate a transcript image of a

3. tissue or cell type, for detecting differences in the chromosomal
 ö
 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY 120
 EVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTW 180
 EVEISITÖDTFTGEKTINLTVÖVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTW 180
 LKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSS 240
 LKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSS 240
 9
 Novel human immunoglobulin superfamily polypeptide, useful in diagnosis, prevention or treatment of immune system, neurological, developmental, muscle and cell proliferative disorders.
 location due to translocation, inversion among normal, carrier or affected individuals, and as hybridisation probes for mapping naturally
 1 MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST
 1 MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST
 Gaps
 Thangavelu K, Ramkumar J;
Arvizu C, Yao MG;
/note= "Antigen precursor signal immunoglobulin fold
glycoprotein T cell surface transmembrane"
 ö
 ; DB 5; Length 298; 4.2e-99;
 0; Indels
 /label= Immunoglobulin domain
 /label= Immunoglobulin_domain
 243. .263
/label= Transmembrane_domain
 69.4%; Score 1472; D
100.0%; Pred. No. 4.2
ive 0; Mismatches
 Elliott VS,
Gandhi AR,
 Claim 1; Page 109-110; 122pp; English
 15-NOV-2001; 2001WO-US044974
 L6-NOV-2000; 2000US-0249645P
 (INCY-) INCYTE GENOMICS INC
 Ή'κ'
 occurring genomic sequences
 .219
 Lu DAM, Yue
P, Gururajan
 Matches 291; Conservative
 2002-519384/55.
 Similarity
 N-PSDB; AAD36780.
 Sequence 298 AA;
 WO200240671-A2.
 LO TP,
 Baughn MR,
 61
 121
 181
 61
 121
 Query Match
 Local
 Domain
 Domain
 Domain
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The invention relates to novel isolated polynucleotides and polypeptides encoded by them. Also included are mutants or variants of the polynucleotides and polypeptides. A polypeptide of the invention has virucide, anti-HIV, cytostatic, antilinlammatory, antiallergic, immunosuppressive, antiarteriosclerotic, hypotensive, osteopathic, haemostatic, antidiabetic, not cardiant activity. The composition and methods are useful in diagnostics, forensics, gene or chromosome mapping, identification of mutations responsible for genetic disorders or other traits, in assessing biodiversity, or in producing many other types of data and products dependent on DNA and amino acid sequences. They may in the composition of the
 immunosuppressive, antiarteriosclerotic; hypotensive, osteopathic; antianaemic; neuroprotective, nootropic; antiparkinsonian; antiasthmatic; haemostatic; antidiabetic; cardiant; HIV; viral infection; cancer; inflammation; allergy; graft rejection; atherosclerosis; hypertension; osteoporosis; anaemia; Alzheimer's disease; Parkinson's disease; asthma; diabetes; myocardial infarction; haemophilia.
 New isolated polypeptides and polynuclectides useful in diagnostics, forensics, in preventing or treating diseases such as HIV and cancer, and as drug targets.
 also be used in preventing or treating diseases (e.g. HIV and other viral infections, cancer, inflammation, allergies, graft rejection, atherosclerosis, hypertension, osteoporosis, anaemia, Alzheimer, disease, parkinson's disease, asthma, diabetes, myocardial infarction or haemophilia). They may also be used as targets in drug screening. The present sequence represents a polypeptide of the invention.
 human; virucide; anti-HIV; cytostatic; antiinflammatory; antiallergic;
291
 241 LYIILSTGGIFLLVTLVTVCACWKPSKRKQKKLEKQNSLEYMDQNDDRLKP
 241 LYIILSTGGIFLLVTLVTVCACWKPSKRKQKKLEKQNSLEYMDQNDDRLKP
 Tang YT;
 Wehrman T, Wang ZW,
 Claim 10; SEQ ID NO 4; 205pp; English.
 ADO47887 standard; protein; 270 AA
 09-JUL-2003; 2003WO-US021703.
 12-JUL-2002; 2002US-0395402P.
 Human protein SEQ ID NO:4.
 Wang J, Zhou P,
 (first entry)
 2004-122914/12.
 (NUVE-) NUVELO INC.
 N-PSDB; ADO47886
 Sequence 270 AA;
 WO2004007672-A2.
 Homo sapiens.
 15-JUL-2004
 22-JAN-2004
 ADO47887;
 Rupp F,
 AD047887
 RESULT
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Gaps

.. 0

Indels

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63.7%; Score 1352; DB 8; 100.0%; Pred. No. 2.1e-90;

100.0%; Pred. No.

Conservative

Matches 268;

8

Local

Query Match

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Similarity

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1 MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST

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180
 240
 The invention relates to a novel isolated polynucleotide and the encoded polypeptide. The molecules of the invention demonstrate antinflammatory, neuroprotective, antianaemic, cytostatic and vulnerary activities and may be useful in preparing a composition for diagnosing or treating inflammatory, haematopoietic, immune, neurodegenerative or stem cell disorders, such as aplastic anaemia or cancer, as well as for promoting wound healing. The molecules may also be utilised during gene therapy procedures. The current sequence is that of a human therapeutic protein of the invention. The current sequence is not shown explicitly within the specification but can be accessed from the WIPO web-site.
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 antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary; inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell; aplastic anaemia; cancer; wound healing; gene therapy.
 LKDGKPLINDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKTTVYRRS
 Z, Ma Y;
Weng G, Zhou
MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST
 EVEISITODTFTGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTW
 New polynucleotide, useful in preparing a composition for diagnosing treating inflammatory, neurodegenerative or stem cell disorders, e.g. aplastic anemia or cancer for promoting wound healing.
 J, Wehrman T, Wang, Ghosh M, Xue AJ,
 LYIILSTGGIFLLVTLVTVCACWKPSKR 268
 Claim 20; SEQ ID NO 1292; 718pp; English.
 Human therapeutic protein - SEQ ID 1292,
 Zhang J,
Wang J,
 Ź
 ADS11055 standard; protein; 270
 30-SEP-2003; 2003WO-US030720.
 02-OCT-2002; 2002US-0416186P.
 г,
 Asundi V, Ren F,
Chen R, Zhao QA,
 WPI; 2004-668857/65.
N-PSDB; ADS10371.
 (NUVE-) NUVELO INC.
 Sequence 270 AA;
 WO2004080148-A2.
 Homo sapiens,
 16-DEC-2004
 23-SEP-2004.
 241
 ΥΤ,
D,
 61
 61
 121
 121
 181
 ADS11055;
 181
 241
 Tang
 ADS11055
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180
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 120
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 180
 The present invention provides the protein and coding sequences of a novel human immunoglobulin domain-containing cell surface recognition molecule known as INSP052. The polypeptide is useful as immunoglobulin domain-containing cell surface recognition molecule. The sequences may also be used in therapy or diagnosing a disease or in the manufacture of a medicament for treating a disease. The disease or in the manufacture of autoimmune/inflammatory, cardiovascular, neurological, psychiatric, developmental, genetic or metabolic disorder, an infection or other pathological condition. The polypeptides and nucleic caids are essential to the structural integrity and homeostatic functioning of most tissues. The present sequence is a polypeptide shown in the invention
 9
 9
 New INSP052 polypeptides and nucleic acids, useful in diagnosing and treating cell proliferative, autoimmune/inflammatory, cardiovascular, neurological, psychiatric, developmental, genetic or metabolic disorder.
 61 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY
 1 MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST
 121 EVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTW
 121 EVEISITDDFFTGEKTINLIVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTW
 181 LKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSS
MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST
 61 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY
 INSP052; human; cell proliferation; autoimmune disease; inflammatio cardiovascular disease; neurological disease; psychiatric disease; developmental disease; metabolic disorder; infection; inmunoglobulin domain-containing cell surface recognition molecule.
 ΰ
 Power
 INSP052 extracellular domain protein.
 ż
 Phelps CB,
 ABG75380 standard; protein; 246
 30-APR-2003; 2003WO-GB001851
 30-APR-2002; 2002GB-00009884.
 Claim 1; Fig 7; Opp; English.
 22-APR-2004 (first entry)
 (ARES-) ARES TRADING SA
 Fagan RJ,
 WPI; 2003-903655/82.
N-PSDB; ACH01279.
 WO2003093316-A2.
 Unidentified
 13-NOV-2003.
 Davids AR,
 ABG75380;
 RESULT 11
ABG75380
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Sequence 246 AA;

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Gaps

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Length 270;

63.7%; Score 1352; DB 8; Length 27 100.0%; Pred. No. 2.1e-90; .ive 0; Mismatches 0; Indels

Query Match 63.7 Best Local Similarity 100. Matches 268; Conservative

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ö
 * isolated polypeptides and polynucleotides useful in diagnostics, rensics, in preventing or treating diseases such as HIV and cancer, and drug targets.
 LKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCRVENPISQGRSLPVKITVYRRSS 240
 human; virucide; anti-HIV; cytostatic; antiinflammatory; antiallergic; immunosuppressive; antiatreriosolerotic; hypotensive; osteopathic; antianaemic; neuroprotective; nootropic; antiaraemic; neuroprotective; nootropic; antiaraemic; neuroprotective; nootropic; antiaraemic; antiasthmatic; haemostatic; antidiabetic; cardiant; HIV; viral infection; cancer; haemostatic; antidiabetic; cardiant; HIV; viral infection; cancer; osteoporosis; ansemia; Alzheimer's disease; Parkinson's disease; asthma; diabetes; myocardial infarction; haemophilia.
 The invention relates to novel isolated polynucleotides and polypeptides encoded by them. Also included are mutants or variants of the polynucleotides and polypeptides. A polypeptide of the invention has virucide, anti-HIV, cytostatic, antiinflamatory, antiallergic, immunosuppressive, antiarteriosclerotic, hypotensive, osteopathic, antianaemic, neuroprotective, nootropic, antiparkinsonian, antiasthmatic, haemostatic, antidaberic, and cardiant activity. The composition and methods are useful in diagnostics, foreniscs, gene or chromosome mapping, identification of mutations responsible for genetic disorders or other traits, in assessing biodiversity, or in producing many other types of
 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY 120
 EVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTW 180
 9
 MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST
 1 MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST
 Gaps
 ö
 Length 246;
 Core 1205,
Pred. No. 1e-79,
Ored. No. 1e-79,
 Tang YT;
 Wang ZW,
 100.0%; Pred.
 Wehrman T,
 Claim 10; SEQ ID NO 7; 205pp; English.
 ADO47890 standard; protein; 237 AA
 Human mature protein SEQ ID NO:7.
 New isolated polypeptides and
 12-JUL-2002; 2002US-0395402P
 09-JUL-2003; 2003WO-US021703
 56.8%;
 ٦,
 (first entry)
Query Match
Best Local Similarity 100.
Matches 240; Conservative
 Shou
 WPI; 2004-122914/12.
 (NUVE-) NUVELO INC
 Rupp F, Wang J,
 N-PSDB; ADO47888
 WO2004007672-A2.
 forensics, in
 Homo sapiens
 15-JUL-2004
 22-JAN-2004
 61
 121
 181
 ADO47890;
 61
 ADO4789
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data and products dependent on DNA and amino acid sequences. They may also be used in preventing or treating diseases (e.g. HIV and other viral infections, cancer, inflammation, allergies, graft rejection, atherosclerosis, hypertension, osteoporosis, anaemia, Alzheimer's disease, Parkinson's disease, asthma, diabetes, myocardial infarction or haemophilla). They may also be used as targets in drug screening. The present sequence represents a polypeptide of the invention.
 213
 121 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRWLLSPDQKVLTITRVLMEDDD 180
 94 DYRDRIRLFENGSLILSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVA 153
 respiratory; cytostatic; antiarthritic; antiinflammatory; gastrointestinal; antibacterial; immunosuppressive; antidiabetic; antirheumatic; gene therapy; molecular weight marker; chromosome marker; chromoseme tag; genetic fingerprinting; nutritional supplement; cancer; inflammatory condition; arthritis; inflammatory bowel disease; crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1; graft versus host disease; human.
 New isolated polynucleotides and polypeptides, useful for treating, e.g. cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease, Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft
 93
 9
 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD
 34 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 1 VNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP
 Gaps
 LYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLLVTLVTVCACWKPSKR
 ö
 Wang J;
 Length 237;
 Indels
 Ä
 F, Xue
Wang Z;
 ö
 56.2%; Score 1192; DB 8;
100.0%; Pred. No. 8.5e-79;
iive 0; Mismatches 0;
 Ren
 IG, Zhang J, Ren
Wang D, Zhao QA,
 Ş
 ADM87341 standard; protein; 256
 21-JUL-2001; 2001US-0306971P.
28-MAR-2002; 2002US-00112944.
 19-JUL-2002; 2002WO-US022858
 Human protein SEQ ID NO:434.
 (first entry)
 Ouery Match
Best Local Similarity 100.
 Weng
 Yang Y, Weng
Ghosh MJ,
 2004-143291/14.
 versus host disease.
 (NUVE-) NUVELO INC.
 N-PSDB; ADM87097
 Sequence 237 AA;
 WO2004009834-A2
 Homo sapiens
 Tang YT, Ya
Wehrman T,
 03-JUN-2004
 29-JAN-2004
 61
 154
 214
 ADM87341;
 888888888888
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Human EST encoded protein SEQ ID NO: 1763.
 12-OCT-2001 (first entry)
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 The present invention describes an isolated polymucleotide (1): (a)

comprising a nucleotide sequence selected from SEO ID NO:1-24; or (b)

which encodes a polypeptide with biological activity, where the

polymucleotide hybridises to (1) under stringent hybridisation conditions

cor has greater than 99 as sequence identity with (1). (1) has respiratory,

cytostatic, antiarthritic, antiinflammatory, gastrointestinal,

antibacterial, immunouppressive, antidiabetic and antirheumatic

cutivities, and can be used in gene therapy. (1) can be used for

generating polymucleotides encoding chimeric or fusion proteins and

heterologous protein sequences. The polymucleotides can be used to

cytosteric protein for ranalysis, characteriation or therapeutic

cytosterions; to compare with endogenous DNA sequences in patients to

compare with endogenous DNA sequences in patients to

dentify potential genetic disorders; as probe to subtract-out known

sequences in the process of discovering other novel polymucleotides; for

confidentify potential genetic disorders; as probe to subtract-out known

sequences in the process of discovering other novel polymucleotides; for

compare including for examination of expression patterns; to raise anti-

protein antibodies using DNA immuniaation techniques; and as an antigen

consupplements, e.g. as a protein or amino acid supplement, as a carbon

consupplements, e.g. as a protein or amino acid supplement, as a carbon

consupplements, e.g. as a protein or amino acid supplement, as condounced

convection or regeneration and treatment of lung or liver fibrosis,

compositions are useful for promoting better or faster closure of non-

consupplements, e.g. as a protein or amino acid supplement, as a curron

convection or regeneration and treatment of lung or liver fibrosis,

compositions are useful for promoting better or faster closure of non-

consupplements, e.g. as a protein or amino acid supplement, and an acid and treatment of lung or liver denses or compared inflammatory conditions (e.g.
 ö
 61 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY 120
 this patent were obtained from the USPTO web site from an equivalent atent US20040048249A1.
 9
 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY
 1 MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST
 1 MKKERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST
 Gaps
 .
0
 56.0%; Score 1189; DB 8; Length 256; 96.7%; Pred. No. 1.6e-78; ive 5; Mismatches 3; Indels (
20; SEQ ID NO 434; 591pp; English
 Sequence 256 AA;
 61
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EVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTW 180
 LKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSS 240
 Best Local Similarity 96.7
Matches 236, Conservative
 241 LYII 244
 241 FYİİ 244
 181
 121
Query Match
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RESULT

AAM24238 standard; protein; 256 AA.

RESULT 14 AAM24238 ID AAM2 XX AC AAM2

AAM24238

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Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
 120
 120
 121 EVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTW 180
 121 EVEISITDDTFTGEKTINLTVDVPISRPQVLGASTTVLELSEAFTLNCSHENGTKPSYTW 180
 240
 240
 The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, bicensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention
 9
 9
 181 LKDGKPLINDSRMLLSPDQKVLTITRVIMBDDDLYSCMVBNPISQGRSLPVKITVYRRSS
 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY
 1 MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST
 MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST
 Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use.
 Gaps
 ;
0
 Asundi
 55.5%; Score 1178; DB 4; Length 256; 97.1%; Pred. No. 9.9e-78; Live 4; Mismatches 3; Indels (
 Chen R,
 7,
 ou P, Qian XB, Wang
Zhang J, Werhman T;
 Claim 20; Page 1159-1160; 1275pp; English.
 25-JAN-2001; 2001WO-US002687.
 17-JUL-2000; 2000US-00617746.
03-AUG-2000; 2000US-00631451.
15-SEP-2000; 2000US-00663870.
 25-JAN-2000; 2000US-00491404
 Zhou P,
 Best Local Similarity 97.1
Matches 234; Conservative
 WPI; 2001-476164/51.
N-PSDB; AAH98897.
 Cao Y, Drmanac RA,
 (HYSE-) HYSEQ INC
 Liu C,
 Sequence 256 AA;
 WO200154477-A2.
 241 L 241
 L 241
 17-JUL-2000;
03-AUG-2000;
 Homo sapiens
 02-AUG-2001
 61
 241
 YT,
 Query Match
 Tang
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the present introduced describes an isolated polymouscoiled (b) (b) comprising a nucleotide sequence selected from SEQ ID NO:1-244; or (b) which encodes a polypeptide with biological activity, where the comprising a nucleotide hybridises to (I) under stringent hybridisation conditions or has greater than 99% sequence identity with (I). (I) has respiratory, cytostatic, antiaribritic, antinilammatory, gastrointestinal, antiaribrities, and antirheumatic activities, and can be used in gene therapy. (I) can be used for activities, and can be used in gene therapy. (I) can be used for generating polymucleotides encoding chimeric or fusion proteins and heterologous protein sequences. The polymucleotides can be used to cypress recombinant protein for analysis, characterisation or therapeutic use; as markers for tissues in which the corresponding protein is chromosome markers or tags to identify chromosome and reads as molecular weight markers on gels; as chromosome markers or tags to identify chromosome and partients to compare with endogenous DNA sequences in patients to genes, related DNA sequences; as probes to hybridise and discover genes, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to subtract-out known sequences in the process of discovering other novel polymucleotides in the process of discovering other novel polymucleotides and polypeptides can also be used as mutritional sources to raise anti-DNA antibodies or elicit another immune response. The polymucleotides and polypeptides can also be used as an utritional source, as a nitrogen source or as a source of carbohydrates. The source, as a nitrogen source or as a source of carbohydrates. The compositions are useful for promoting better or faster closure of norce compositions are useful for promoting abetter or faster closure of norce compositions are useful for promoting better or faster closure of norce compositions are useful and regeneration of tissues, for protecting and area and an analyse o
 respiratory; cytostatic; antiarthritic; antiinflammatory; agastrointestinal; antibacterial; immunosuppressive; antidiabetic; antitheumatic; gene therapy; molecular weight marker; chromosome marker; chromosome tag; genetic fingerprinting; nutritional supplement; cancer; inflammatory condition; arthritis; inflammatory bowel disease; croh"s disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1; graft versus host disease; human; expressed sequence tag; EST.
 New isolated polynucleotides and polypeptides, useful for treating, e.g. cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease, Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft
 The present invention describes an isolated polynucleotide (I): (a)
 Wang J;
 Xue A,
 Human EST derived amino acid sequence SEQ ID NO:880
 Zhang J, Ren F, Xue
D, Zhao QA, Wang Z;
 Example 2; SEQ ID NO 880; 591pp; English.
 ADM87787 standard; protein; 256 AA
 19-JUL-2002; 2002WO-US022858.
 21-JUL-2001; 2001US-0306971P.
28-MAR-2002; 2002US-00112944.
 Wang
 Yang Y, Weng G,
, Ghosh MJ, Wang
 (first entry)
 WPI; 2004-143291/14.
 versus host disease.
 (NUVE-) NUVELO INC.
 N-PSDB; ADM87569
 402004009834-A2
 Homo sapiens
 03-JUN-2004
 29-JAN-2004.
 Tang YT, Y
 ADM87787;
ADM87787
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reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage. The compositions can also be used to treat inflammatory conditions (e.g. arthritis, inflammatory bowel disease or Crohn's disease), sepsis, rheumatoid arthritis, diabetes mellitus type or graft versus host disease. The present sequence represents an expressed sequence tag (EST) derived amino acid sequence from the present invention. N.B. The sequences for this patent were obtained from the USPTO web site from an equivalent US patent US20040048249A1. ö 121 EVELSITIDDIPPIGEKTINLIVDVPISRPQVLVASTIVLELSEAFTLNCSHENGIKPSYTW 180 240 61 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY 120 120 9 9 1 MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST 1 MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY 181 LKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSS Gaps ó 55.5%; Score 1178; DB 8; Length 256; 97.1%; Pred. No. 9.9e-78; ive 4; Mismatches 3; Indels ( Search completed: July 26, 2005, 16:07:32 Job time : 120.106 secs Matches 234; Conservative Query Match Best Local Similarity Sequence 256 AA; 241 L 241 241 L 241 8888888888888 셤 ò g ò g ò 셤 ò 유

GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd. Copyright

 protein search, using sw model OM protein July 26, 2005, 15:58:02 ; Search time 24.0385 Seconds Run on:

(without alignments) 1665.085 Million cell updates/sec

US-10-706-691-16 2122 1 MKRERGALSRASRALRLAPF.....TAGVHIIREQDEAGPVEISA 416

Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 8 08 Minimum | Maximum |

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl: \* 2: pirl: \* 3: pirl: \* 4: pir4: \* PIR 79:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARIES

|               |       | d              |        |    | SUMMAKIES |                    |
|---------------|-------|----------------|--------|----|-----------|--------------------|
| Result<br>No. | Score | Query<br>Match | Length | DB | aı        | Description        |
|               |       |                | -      | •  |           | •                  |
| -             | 770   | * · O T        |        | 4  | KWHOCZ    |                    |
| 7             | 216   | 10.2           |        | ~  | JC1512    | biliary glycoprote |
| ო             | 207.5 | 9.6            |        | ~  | JC1506    | biliary glycoprote |
| 4             | 202.5 | 9.5            |        | 7  | A39037    | carcinoembryonic a |
| ß             | 197.5 | 9.3            | 365    | ~  | JC7780    | coxsackie- and ade |
| ø             | 194.5 | 9.5            |        | ~  | T17346    | hypothetical prote |
| 7             | 189   | 8.9            |        | ~  | I48268    | glyco              |
| œ             | 188.5 | 8.9            | _      | ~  | A58532    | glial cell membran |
| 6             | 188   | 8.9            |        | ~  | JC1511    | biliary glycoprote |
| 10            | 186.5 | 8.8            |        | ~  | JC1509    | biliary glycoprote |
| 11            | 183.5 | 9.8            |        | 7  | A46500    | Ly-9.2 antigen - m |
| 12            | 181.5 | 8.6            |        | 7  | S34338    | biliary glycoprote |
| 13            | 180.5 |                |        | 7  | S41638    |                    |
| 14            |       | 8.5            | 278    | ~  | JC1507    | biliary glycoprote |
| 15            | 178.5 | 8.4            |        | ~  | A54879    | pregnancy-specific |
| 16            | 173.5 |                |        | -  | RWRIC2    | T-cell surface gly |
| 17            | 173.5 | 8.2            |        | Н  | IJBONC    | neural cell adhesi |
| 18            | 173   | 8.2            |        | N  | S56749    | junctional adhesio |
| 19            | 172.5 | 8.1            |        | -  | IJRTNC    | neural cell adhesi |
| 20            | 170.5 | 8.0            |        | н  | A32164    | biliary glycoprote |
| 21            | 170.5 | 8.0            |        | N  | T23004    | hypothetical prote |
| 22            | 168.5 | •              |        | ~  | I76668    |                    |
| 23            | 168   | 7.9            |        | Н  | IJHONG    | neural cell adhesi |
| 24            | 166   | 7.8            | 458    | ~  | S68177    | C-CAM2a protein is |
| 25            | 166   | 7.8            |        | ~  | S23969    | cell-adhesion mole |
| 56            | 166   | 7.8            | 519    | ~  | A44783    | ecto-ATPase precur |
| 27            | 166   | 7.8            |        | Н  | IJCHNL    | neural cell adhesi |
| 28            | 164   | 7.7            | 464    | ~  | C30127    |                    |
| 59            | 163.5 | 7.7            | 725    | ~  | JE0100    | neural cell adhesi |

| biliary glycoprote | neural cell adhesi | biliary glycoprote | neural cell adhesi | neural cell adhesi | neural cell adhesi | nonspecific cross- | carcinoembryonic a | biliary glycoprote | biliary glycoprote | biliary glycoprote | pregnancy-specific | pregnancy-specific | pregnancy-specific | pregnancy-specific | pregnancy-specific |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| 1508               | MSNL               | 4SR1               | 0635               | 43027              | JMSNG              | 27681              | A35364             | H0395              | 10396              | H0394              | 13354              | 3354               | 3354               | 3354               | 43354              |
| S,                 | 5                  | Z                  | 5                  | Ě                  | Ĥ                  | 4                  | ⋖                  | 5                  | 5                  | 5                  | ß                  | F4                 | ¥                  | H4                 | Ω                  |
| 2 30               | 1.5                | 1 WM               | 5                  | 7                  | ī                  | 2<br>A             | 7<br>7             | 2                  | 2                  | ر<br>د             | 2<br>G             | 2 F4               | 2 A4               | 2 H4               | 2                  |
| 7                  | Н                  | -                  | -                  | 0                  | н                  | 0                  | 7                  | 7                  | ~                  | 417 2 JJ           | ~                  | ~                  | 0                  | ~                  | ~                  |
| 521 2              | 1115 1             | 458 1              | 1092 1             | 1232 2             | 725 1              | 344 2              | 709 2              | 321 2              | 351 2 ,            | ~                  | 324 2 (            | 326 2              | 333 2              | 335 2 ]            | 406 2              |
| 7.7 521 2          | 7.6 1115 1         | 7.6 458 1          | 7.6 1092 1         | 7.6 1232 2         | 7.5 725 1          | 7.5 344 2          | 7.5 709 2          | 7.4 321 2          | 7.4 351 2          | 417 2              | 7.4 324 2 (        | 7.4 326 2          | 7.4 333 2          | 7.4 335 2 ]        | 406 2              |

## ALIGNMENTS

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surface glycoprotein CD2 precursor - human

NiAlternate names: Erosette receptor; erythrocyte receptor; erythrocyte-binding protein C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Saccession: A28967; A26486; B26486; A28023; S03239; A30430; S00829; A29874
C; A3ccession: A28967; A26486; B26486; A28023; S03239; A30430; S00829; A29874
R; Diamond, D.J.; Clayton, L.K.; Sayre, P.H.; Reinherz, B.L.
Proc. Natl. Acad. Sci. U.S.A. 85, 1615-1619, 1988
A; Title: Exon-intron organization and sequence comparison of human and murine T11 (CD2)
A; Reference number: A28967; MUID:88144486; PMID:2894031

A,Molecule type: DNA A,Residues 1.351 - CDIA. A;Cross-references: UNIRROT:P06729; GB:M19806; GB:J03622; GB:J03623; NID:g180079; PIDN:A, R;Sewell, W.A.; Brown, M.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J. Proc. Natl. Acad. Sci. U.S.A. 83, 8718-8722, 1986 A;Title: Molecular cloning of the human T-lymphocyte surface CD2 (T11) antigen. A;Reference number: A26486; MUID:87041523; PMID:3490670

A; Accession: A26486

A:Molecule type: mRNA A;Residues: 1-338,'M',340,'QQKTHCPLPLIKKDRNCLFQ' <SE1> A;Accession: B26486

A;Molecule type: protein
A;Residues: 25-46,'X',50 <SE2>
R;Sewell, W.A.; Brown, M.H.; Dunne, J.; Owen, M.J.; Crumpton, M.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 7256, 1987
A;Reference number: A28416
A;Contents: revision
A;Accession: A28416

A;Molecule type: mRNA A;Residues: 333-351 <SE3> R;Seed, B.; Aruffo, A. Proc. Natl. Acad. Sci. U.S.A. 84, 3365-3369, 1987 Proc. Natl. Acad. Sci. U.S.A. 84, 3365-3369, 1987 A;Title: Molecular cloning of the CD2 antigen, the T-cell erythrocyte receptor, by a rap A;Reference number: A28023; MUID:87204137; PMID:2437578

A; Molecule type: mRNA

A;Residues: 1-265, Q',267-351 <SEE>
A;Cross-references: GB:ML6445; NID:g178668; PIDN:AAA51738.1; PID:g178669
A;Cross-references: GB:ML6445; NID:g178668; PIDN:AAA51738.1; PID:g178669
B;Sayre, P.H.; Chang, H.C.; Hussey, R.E.; Brown, N.R.; Richardson, N.E.; Spagnoli, G.; C
Proc. Natl. Acad. Sci. U.S.A. 84, 2941-2945, 1987
A;Title: Molecular cloning and expression of T11 cDNAs reveal a receptor-like structure of A;Reference number: S02292; MUID:87204243; PMID:2883656

A; Accession: S02292

A,Residues: 1-338,'M',340,'QQXTHCPLPLIKKDRNCLFQ' <SA1> A,Cross-references: GB:M16336; NID:g180093; PIDN:AAA51946.1; PID:g180094 A; Molecule type: mRNA

A; Accession: A30430

A;Molecule type: protein A;Residues: 25-43,152-163 <SA2> R;Lang, G.; Wotton, D.; Owen, M.J.; Sewell, W.A.; Brown, M.H.; Mason, D.Y.; Crumpton, M.

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biliary glycoprotein B - mouse
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 73
 C;Genetics:
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EMBO J. 7, 1675-1682, 1988

A; Title: The structure of the human CD2 gene and its expression in transgenic mice.
A; Accession: $00829; MUID:89005055; PMID:2901953
A; Accession: $00829
A; Molecule type: DNA
A; Residues: 1-31 < LANS
A; Cross-references: EMBL:X07871
C; Comment: CD2 is a surface antigen expressed on all peripheral blood T-cells. It appear or is closely associated with, the erythrocyte receptor.
C; Genetics:
A; Gene: GDB:CD2
A; Cross-references: GDB:118735; OMIM:186990
A; Map position: 1p13.1-1p13.1
A; Introns: 21/1; 128A1; 205/1; 246/1
C; Superfamily: T-cell surface glycoprotein CD2
C; Keywords: glycoprotein; T-cell; transmembrane predicted < SIG>F; 25-351/Product: T-cell surface glycoprotein CD2 #status predicted < FXT>F; 210-234/Domain: signal sequence #status predicted < FYMT>F; 210-234/Domain: intracellular #status predicted < TWW*
F; 237-351/Domain: intracellular #status predicted < TWW*
F; 237-351/Domain: intracellular #status predicted < INT>F; 89,141,150/Binding site: carbohydrate (Asn) (covalent) #status predicted
 biliary glycoprotein H - mouse
biliary glycoprotein H - mouse
biliary glycoprotein H - mouse
c;psecises: Mus musculus (house mouse)
c;psecises: Mus musculus (house mouse)
c;psecises: Musculus (house mouse)
c;pacession: JC1512
R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
A;Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopromy. Reference number: JC1505; MUD:93273228; PMID:8500759
A;Accession: JC1512
A;Residues: 1-341 cMCC>
A;Residues: 1-341 cMCC>
A;Cosserveferences: UNIPROT:061354; GB:X67283
C;Comment: This protein is expressed at the cell surface and plays a determinant role in A;Gene: BgpH
 RMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSSLYIILS-TGGI 250
 FLLVTLVTVCACWKPSKRKQKKLEKQNSLEYMDQNDDRLKPEADTLPRSGEGERKNPMAL 310
 268 IPASTPONPATSOHPPPPPGHRSQAPSHRPPPPGHRVOHODOKRPPAPSGTOVHQOKGPP 327
 77 VTVVQSIGTEVIGTLRPD-----YRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTF 131
 132 TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDS 191
 221 SİLMVFVALLVFYITKRKKÖRS------RRNDEELETRAH---RVATEERGRKPHQ 267
 311 YILKDKDSPETEENPAPEPRSATE----PGPPGYSVS-----PAVPG----RSPGLP 354
 17 LAPFVYLLLIQIDPLEGVNITSPVRLIHGTVGKSALLSVQYSSISSDRPVVKWQLKRDKP
 Gaps
 10.4%; Score 220; DB 1; Length 351; 22.9%; Pred. No. 2e-06; cive 60; Mismatches 164; Indels
 Conservative
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LPRPRVQPKPP 338
 355 IRSARRYPRSP 365
 Similarity
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 Query Match
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Matches 8
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C;Species' Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: JC1506
R;McCuaig, K; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.
Gene 127, 173-183, 1993
A;Accession of the Bgp gene and characterization of mouse colon biliary glycoprotication: Expression of the Bgp gene and characterization of mouse colon biliary glycoprotication of mouse: JC1505, MUID:93273228; PMID:8500759
A;Accession: JC1506
A;Status: nucleic acid sequence not shown
A;Status: nucleic acid sequence not shown
A;Residues: 1-278 +MCC.
 C;Superfamily: biliary glycoprotein; carcinoembryonic antigen precursor amino-terminal hor
C;Kbywords: glycoprotein; receptor
F;1-138/bomain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;18-216/Domain: immunoglobulin homology <IrWMs
F;87,104,153,195/Binding site: carbohydrate (Asn) (covalent) #status predicted
Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termine
 A; Cross-references: UNIPROT: Q99232
C; Comment: This protein is expressed at the cell surface and plays a determinant role in
 <CEAN>
 Š,
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 128
 244
 185 QLTERMILISQNNSILLRIDPIKREDAGEYQCEISNPVSVKRSNSIKLDI------IFDPT 237
 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITD 128
 DTF-TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPL 187
 (covalent) #status predicted
 DIF-TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPL 187
 ---LSTG-----GIFLLVTLVTVCACWKPSKRKQKKLEKQNSLEYMDQNDDRLKPEAD 294
 C;Keywords: glycoprotein; receptor
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology
F;159-216/Domain: immunoglobulin homology <IMM>
F;87,104,153,195/Binding site: carbohydrate (Asn) (covalent) #status predic
 73 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITD
 LNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSSLYII---
 Gaps
 9;
 Query Match 10.2%; Score 216; DB 2; Length 341; Best Local Similarity 26.1%; Pred. No. 3.4e-06; Matches 73; Conservative 48; Mismatches 125; Indels 34;
 LNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITV 235
 Length 278;
 Indels
 295 TLPRSGEQERKNPMALYILKDKDSPETEENPAPEPRSATE 334
 Query Match
9.8%; Score 207.5; DB 2;
Best Local Similarity 32.1%; Pred. No. 8.8e-06;
Matches 54; Conservative 32; Mismatches 73;
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332
 188 LNDSRML-----LSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRS 239
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 279 -------EDVPPPKSRTSTARSYIGSNHSSLGSMSPSNME 311
 52 VKIDDAGVY----SCTAQNSAGSISANATLTVLETPSLVVPLEDRVVSVGETVALQCRAT 107
 231
 GNPPPRITWFKGDRPLSLTERHHLTPDNQLLVVQNVVAEDAGRYTCEMSNTLGTERA--- 164
 KITVYRRSSLYIILSTG-----GIF-----LLVTLVTVCACWKPSKRKQKKLEK 275
 214 ----EYSVINTDETVVPPDVPSYLSSQGTLSDRQETVVRTEGGPQANGHIESNGVCPRDA 269
127 G--VGNKKIQLTVLVKPSGIRCYVDGSE--BIGNDFKLKCEPKEGSLPLRYEWQK---- 177
 112 LQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHE 171
 270 SHFPEPDTHSVACRQPKLCAGSAYHKEPWKAMEKAEGTPGPHKMEHGGRVVCSDCNTEVD 329
 21
 Cispecies: Homo sapiens (man)
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 240 S----LYIILSTGGIFLLVTLVTVCACWKPSKRKOKKLEKONSLEYMDQNDDRLKPEAD
 TLPRSGEQERKNPMALYILKDKDSPETEENPAPEPRSATEP---GPPGYSVSPAVPGRSP
 55 VQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLF---ENGSLLLSD
 NGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPV
 QNSLEYMDQNDDRLKPEADTLPRSGEQERKNPMALYILKDKDSPETE---ENPAPEPRSA
 93;
 9.2%; Score 194.5; DB 2; Length 483; llarity 21.5%; Pred. No. 0.00011; Conservative 55; Mismatches 155; Indels 93;
 352 G-----LPIRSARRYPRSPARSPATGRTHSSPPRAPSSPGRSR 389
 312 GYSKTQYNQVPSEDLERAPQSP-----TLPPAKVAAPNLSR 347
 hypothetical protein DKFZp58601624.1 - human (fragment)
 333 TE-PGPPGYSVSPAVPGRSPGL-----PIRSARR-----
 361 -YPRSPARSPATGRIHSSPPRAPSSP 385
 CYSRGQAFHPQPVSRDSAQPSAPNGP 355
 148268
biliary glycoprotein - mouse
 Query Match
Best Local Similarity
Matches 83; Conserv
 C,Genetics:
A,Note: DKFZp58601624.1
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 Carcinoembryonic antigen mmCGM2 precursor - mouse

N;Alternate names: biliary glycoprotein homolog; calcium-dependent cell adhesion molecul
C;Species: Mus musculus (house mouse)
C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 09-Jul-2004
C;Accession: A39037; S13760
C;Accession: A39037; M.; Stanners, C.P.; Beauchemin, N.
J. Biol. Chem. 266, 309-315, 1391
A;Title: A mouse carcinoembryonic antigen gene family member is a calcium-dependent cell
A;Reference number: A39037; MUD:91093141; PMID:1985902
A;Accession: A39037
A;Molecule type: mRNA
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A;Accession: A39037
A;Molecule type: mRNA
A;Reficence UNIPROT:099232; GB:X53084; NID:550368; PIDN:CAA37251.1; PID:950369
C;Superfamily: biliary glycoprotein; carcinoembryonic antigen precursor amino-terminal homology «CEAN»
F;1-134/Domain: signal sequence #status predicted «STC»
F;1-134/Domain: signal sequence #status predicted «EXT»
F;35-278/Product: carcinoembryonic antigen mmCGM2 #status predicted «TMM»
F;25-216/Domain: immunoglobulin homology «ITMM»
F;35-228/Domain: inmunoglobulin homology «ITMM»
F;269-278/Domain: intracellular #status predicted «ITM»
F;87-278/Domain: intracellular #status predicted «ITM»
F;87-278/Domain: intracellular #status predicted «ITM»
F;87-278/Domain: intracellular #status predicted «ITM»
F;87-104,153,195/Binding site: carbohydrate (Asn) (covalent)
 JC7780

Coxaackie- and adenovirus receptor - bovine

C;Species Bos primigenius taurus (cattle)

C;Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 09-Jul-2004

C;Accession: JC7780

C;Accession: JC7780

C;Accession: JC7780

C;Accession: JC7780

C;Accession: JC7780

A;Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus recepton A;Reference number: JC7780
 cella
 on bovine
 20;
 KGNPVSTNAEIVHFVTGTNKTTTGPAHSGRETVYSNGSLLIQRVTVKDTGVYTIE--MTD 126
 DIF-TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPL 187
 79 VVQSI----GTEVIGTLRPDYRDRIRLFEN-----GSLLLSDLQLADEGTYEVEISITD 128
 .29 DTFTGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKP-SYTWLKDGKPL 187
 22 YLLLI-QTDPLEGVNITSPVRLIHGTVGKSALLSVQYSSTSSDR-PV-VKWQLKRDKPVT 78
 73 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITD
 A;Cross-references: UNIPROT:Q8WMV3; GB:AY033651
C;Comment: This protein serves as the primary adenoviral attachment site
 9.3%; Score 197.5; DB 2; Length 365; 23.6%; Pred. No. 5.1e-05; tive 64; Mismatches 143; Indels 103;
 9
 Query Match 9.5%; Score 202.5; DB 2; Length 278; Best Local Similarity 32.1%; Pred. No. 1.8e-05; Matches 54; Conservative 31; Mismatches 74; Indels 9;
 QLTERMILSQNNSILRIDPIKREDAGEYQCEISNPVSVKRSNSIKLDI 232
 188 INDSRMILSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITV 235
 96; Conservative
 Similarity
 A; Molecule type: mRNA
A; Residues: 1-365 <THO>
 A; Contents: Liver
A; Accession: JC7780
 69
 129
 Matches
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ENPAPEPRSATEPG 336
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940 YHPQPVPRDSGQPG 953
 Query Match
Best Local Similarity 25.2*
Matches 64; Conservative
 glycoprotein G - mouse
 265 PSKRKQK------
 A; Residues: 1-341 <MCC>
 A; Molecule type: DNA
 C; Accession: JC1511
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 286
 323
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 C;Genetics:
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 A58532

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C;Species: Mus musculus (house mouse)

C;Apecies: Mus musculus (house mouse)

C;Apecies: Mus musculus (house mouse)

C;Apecies: Mus musculus (house mouse)

C;Accession: A58532

R;Suzuki, Y; Sato, N; Tohyama, W; Wanaka, A.; Takagi, T.

J Biol. Chem. 271, 2252-22527, 1996

A;Fitle: cDNA cloning of a novel membrane glycoprotein that is expressed specifically in A,Reference number: A58532; MUD: 96394313; PMID: 8798419

A;Andecule type: mRNA

A;Residues: L-1091 (2012)

A;Rolecule type: mRNA

A;Residues: 1-1091 (2012)

A;Andecule type: mRNA

A;Residues: 1-1091 (2012)

A;Andecule richalpha-2-glycoprotein repeat homology (LRR1)-

F;71-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology (LRR2)-

F;11-141/Domain: leucine-rich alpha-2-glycoprotein repeat homology (LRR5)-

F;11-150main: leucine-rich alpha-2-glycoprotein repeat homology (LRR5)-

F;11-150main: leucine-rich alpha-2-glycoprotein repeat homology (LRR5)-

F;11-131/Domain: leucine-rich alpha-2-glycoprotein repeat homology (LRR7)-

F;28-261/Domain: leucine-rich alpha-2-glycoprotein repeat homology (LR10)-

F;38-381/Domain: leucine-rich a
C;Species: Mus musculus (house mouse)
C;Date: 0.2-Unl-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Date: 0.2-Unl-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Date: 0.2-Unl-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Date: 0.2-Unl-1996 #sequence_revision 0.2-Jul-1996 #text_change 09-Jul-2004
B;Nedellec, P.; Dveksler, G.S.; Daniels, E.; Turbide, C.; Chow, B.; Basile, A.A.; Holmes
A;Title: Bgp2, a new member of the carcinoembryonic antigen-related gene family, encodes
A;Reference number: A53995; MUID:94267915; PMID:8207827
A;Accession: Idate
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A;
 A.Cross-references: UNIPROT:QRINS; EMBL:X76085; NID:g511020; PIDN:CAA53699.1; PID:g5110

Genetics:
A.Gene: Bgp2
C.Superfamily: biliary glycoprotein; carcinoembryonic antigen precursor amino-terminal h

C.Superfamily: biliary glycoprotein; precincembryonic antigen precursor amino-terminal h

F.Steywords: glycoprotein

F.1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F:159-216/Domain: immunoglobulin homology <IMM>
 71 LKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDT 130
 TGTNKTIK------GPVHSGRETLYSNGSLLIQRVTMKDTGVYTE--MTDQN 128
 131 F-----TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGK 185
 186 PLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSSLYI-- 243
 183 TLLITEKMTTSQAGLILKIDPIKKEDAGEYQCEISNPVSVKRSNSIKLEVIFDSTYDISD 242
 LLASWSPPTTAQVTVMAFPLHAAEGNNVILVVYNMMKGVSAFSWHKGSTTSTNAEIVRFV 83
 24 LLIQTDPLEGVNITSPVRLIHGTVGKSALLSV------QYSSTSSDRPVVKWQ 70
 Gaps
 48;
 Length 272;
 8.9%; Score 189; DB 2; Length 272
25.4%; Pred. No. 0.00012;
tive 46; Mismatches 100; Indels
 :: || |: |
243 VPIAVIITGAVAGVILIAGL 262
 l Similarity 25.4 66; Conservative
 Query Match
 Best Local
 Matches
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A;Gene: BgpG
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
 of mouse colon biliary glycopro
 A; Cross-references: UNIPROF: Q61353; GB: X67282
C; Comment: This protein is expressed at the cell surface and plays a determinant role in
 C; Keywords: glycoprotein; receptor
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;15-124/Domain: immunoglobulin homology <IMM1>
F;159-216/Domain: immunoglobulin homology <IMM2>
F;159-216/Domain: immunoglobulin homology <IMM2>
F;159-216/Domain: immunoglobulin homology <IMM2>
F;71,89,104,153,195/Binding site: carbohydrate (Asn) (covalent) #status predicted
 16;
 : | | | | :: | | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: |
 95 YRDRIRLFENGSLILLSDLQLADEGTYEVEISITDDTF-TGEKTINLTVDVPISRPQVLVA 153
 STTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 213
 45 GTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLF-- 102
 103 -ENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLV-ASTTVLEL 160
 161 SEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVE 220
 NPISQGRSLPVKITVYRRSSLYIILSTG-----GIF-----LLVTLVTVCACWK 264
 820 TRKKSEEYSVTNTDETIVPPDVPSYLSSQGTLSDRQETVVRTEGGHQANGHIESNGVCLR 879
 ----SPETE 322
 C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
 Indels 30; Gaps
 RimcCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N. Gene 127, 173-183, 1993
A;Title: Expression of the Bgp gene and characterization of mouse colon A;Reference number: JC1505; MUID:93273228; PMID:8500759
A;Accession: JC1511
 Indels 117;
F;385-408/Domain: leucine-rich alpha-2-glycoprotein repeat homology F;409-432/Domain: leucine-rich alpha-2-glycoprotein repeat homology F;440-485/Domain: proteoglycan carboxyl-terminal homology <PCH>
 Length 1091;
 Length 341;
 DDRLKPEADTLPRSGEGER----KNPMALYILKDKD---
 Query Match
8.9%; Score 188.5; DB 2;
Best Local Similarity 21.1%; Pred. No. 0.00073;
Matches 79; Conservative 56; Mismatches 122;
 8.9%; Score 188; DB 2; L 25.2%; Pred. No. 0.00018; ative 45; Mismatches 115;
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Cross-references: UNIPROT: Q61352; EMBL:X67281; NID:g312585; PIDN:CAA47698.1; PID:g3125; McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N. and 127, 173-183, 1993
 Molecule type: protein
,Residues: 35-59 <WIL>
,Comment: This protein is expressed at the cell surface and plays a determinant role in
 Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopro; Reference number: JC1505; MUID:93273228; PMID:8500759
 Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
 biliary glycoprotein F - mouse
NyAlternate names: mouse hepatitis virus (MHV) receptor glycoprotein
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: 334338; JC1510; A41093
R;Huang, D.C.; Huang, X.F.; Novel, M.; Novel, G.
submitted to the EMBL Data Library, July 1992
A;Description: A Clp-family gene present on the lactose-protease plasmid of lactococcus A;Accession: 534338
 the carcinoembryonic antigen
 carbohydrate (Asn)
 C;Keywords: glycoprotein; receptor
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;160-219/Domain: immunoglobulin homology <IMM1>
F;254-3103/Domain: immunoglobulin homology <IMM2>
F;339-396/Domain: immunoglobulin homology <IMM2>
F;339-396/Domain: immunoglobulin homology <IMM3>
F;87,104,148,199,206,210,226,258,290,294,304,333,375/Binding site: carbohydrate (
 66 LALVFYKKDITILDKGYNGRLKVSEDGYSLYMSNLTKSDSGSYHAQINQKNVILTTNKEF 125
 126 TLHIYEKLOKPOIIVESVTPSDTDSCTFTLICT-VKGTKDSVQYSWTRE-----DTHLN 178
 19 PFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVT
 14 PLLFLLM----GLGASGKETPPTVISGMLGGSVTFSLNISKDAEIEHII-WNC---PPKA
 79 VVQSIGTEVIGTLRPDYRDRIRLFENG-SLLLSDLQLADEGTYEVEISITDDTFTGEKTI
 138 NLTVDVPISRPQVLVASTTVLEL-SEAFTLNCSHENGTKPS--YTWLKDGKPLLNDSRML
A;Cross-references: GB:M84412; NID:g198931; PIDN:AAA39468.1; PID:g198932
A;Experimental Source: C57BL/6
A;Note: sequence extracted from NCBI backbone (NCBIN:111651, NCBIP:111654)
C;Keywords: transmembrane protein
 Gaps
 Gaps
 19;
 17;
 Length 521;
 Indels
 Indels
 οĘ
 TYDGSHTLRVSQSVCDPDLPYTCKAWNPVSQNSSQPVRI 217
 195 LSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKI, 233
 A.Molecule type: mRNA
A.Residues: 1-81, 'V', 83-141, 'P',143-521 <MCC>
A.fresidues: 1-81, 'V', 83-141, 'P',143-521 <MCC>
A.fresidues: R.K.; Jiang, G.S.; Holmes, K.V.
R.Williams, R.K.; Jiang, G.S.; Holmes, K.V.
Proc. Natl. Acad. Sci. U.S.A. 88, 5533-5536, 1991
A.Title: Receptor for mouse hepatitis virus is a member
A.Reference number: A41093; MUID:91288498; PMID:1648219
 ; Score 183.5; DB 2;
; Pred. No. 0.00074;
43; Mismatches 98;
 8.6%; Score 181.5; DB 2;
27.4%; Pred. No. 0.00077;
ative 37; Mismatches 84;
 26.98;
 Query Match
Best Local Similarity 26.9%
Matches 59; Conservative
 Best Local Similarity 27.49
Matches 52; Conservative
 Molecule type: mRNA
Residues: 1-521 < HUA>
 Status: preliminary
 Status: preliminary
 Accession: JC1510
 Accession: A41093
 179
 Query Match
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 RESULT 10

biliary glycoprotein E - mouse

biliary glycoprotein E - mouse

C;Species: Mus musculus (house mouse)

C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004

C;Accession: JCI509

R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.

R;Accuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.

A;Title: Expression of the Bgp gene and characterization of mouse colon biliary glycopxc

A;Reference number: JCI505; MUID:93273228; PMID:8500759
 Cross-references: UNIPROT: 061351; GB:X67280
Comment: This protein is expressed at the cell surface and plays a determinant role in
 ੁ
 Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
 RESULT 11

1y-9.2 antigen - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A46500
R;Sandrin, M.S.; Gumley, T.P.; Henning, M.M.; Vaughan, H.A.; Gonez, L.J.; Trapani, J.A.;
J Immunol. 149, 1636-1641, 1992
A;Title: Isolation and characterization of cDNA clones for mouse Ly-9.
A;Reference number: A46500; MUID:92373005; PMID:1506686
A;Accession: A46500
A;Accession: A46500
A;Accession: preliminary
A;Acteure preliminary
A;Residues: 1-629 <SAN>
 A Cross-references: UNIPROT:061351; GB:X67280
C; Comment: This protein is expressed at the cell surface and plays a determinant role C; Comment: This protein is expressed at the cell surface and plays a determinant role C; Genetics:
A; Gene: BgpE
C; Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-term C; Superfamily: carcinoembryonic antigen precursor amino-term F;1-138/Domain: carcinoembryonic antigen precursor amino-term F;1-138/Domain: immunoglobulin homology <IMM1>
F;254-303/Domain: immunoglobulin homology <IMM2>
F;354-304/Domain: immunoglobulin homology <IMM3>
F;87,104,148,199,206,210,226,258,290,294,304,333,375/Binding site: carbohydrate (Asn)
 ġ
 ----GIFLLWTLWTVC 260
 ---İFDPTQGGLSDGAIAGIVIGVVAGVALIAGL 263
 73 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITD 128
 DTF-TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNC-SHENGTKPSYTWLKDGKP 186
 : | | : : | : : | : : | : : | : : | 127 ENFRITEATVQFHVHPLLLKPNITSNNSNPVEGDDSVSLTCDSYTDPDNITYLWSRNGES 186
 LLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSSLY---- 242
 187 LSEGDRLKLSEGNRTLTLLNVTRNDTGPYVCETRNPVSVNRSDPFSLNI-----1YGPDT 241
 261 ACWKPSKRKQKKLEKQNSLEYMDQNDDRLKPEADTLPRSGEQERKNPMALYILKDKDSPE
 Gaps
 17;
 Length 458;
 Indels
 DB 2;
 83;
 ch 8.8%; Score 186.5; DB 2
1 Similarity 27.4%; Pred. No. 0.00032;
52; Conservative 38; Mismatches 83
 214 LYSCMVENPISQGRSLPVKITVYRRSSLYII--
 211 EYOCEISNPVSVRRSNSIKLDI--
 319 NRPTSAPSSPRATE 332
 321 TEENPAPEPRSATE 334
 243 IILSTGGIFL 252
 251
 |:| |:|
PIISPSDIYL
 A; Molecule type: mRNA
A; Residues: 1-458 <MCC>
 Query Match
Best Local S
Matches 52
 69
 129
 187
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A)Cross-references: UNITROT:061350; GB:X67278
G;Comment: This protein is expressed at the cell surface and plays a determinant role in C;Comment: This protein is expressed at the cell surface and plays a determinant role in C;Conetics:
A;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: biliary glycoprotein; carcinoembryonic antigen precursor amino-terminal hw C;Keywords: glycoprotein; receptor
F;1-138/Domain: arcinoembryonic antigen precursor amino-terminal homology <CEAN>
F;75-24/Domain: immunoglobulin homology <IMM1>
F;75-216/Domain: immunoglobulin homology <IMM2>
F;159-216/Domain: immunoglobulin homology <IMM2>
F;159-216/Domain: immunoglobulin carbohydrate (Asn) (covalent) #status predicted
 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-475 < CHE>
A;Residues: 1-475 < CHE>
A;CRES-totes: 1-475 < CHE>
A;CRES-totes-teferences: UNIRROT:Q62664; GB:U09815; NID:g497254; PIDN:AAA56870.1; PID:g497255
A;Cross-references: UNIRROT codon GCT for residue 64 as Gly
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
 pregnancy-specific glycoprotein rnCGM3 - rat
pregnancy-specific glycoprotein rnCGM3 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: 19-dan-1996 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
C;Accession: A54879
R;Chen, H.; Chen, C.L.; Chou, J.Y.
B;Chen, H.; Chen, C.L.; Chou, J.Y.
B;Chen, H.; Chen, C.L.; 1994
B;Chen, H.; Chen, C.L.; Thut, Chen, C.L.; A;Ritle: Characterization of two promoters of a rat pregnancy-specific glycoprotein s
A;Reference number: A54879; MUID:94347731; PMID:8068638
 F;1-137/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA1>F;242-378/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEA2>F;399-456/Domain: immunoglobulin homology <IMM2>
 84 GTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDV 143
 YRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTF-TGEKTINLTVDVPISRPQVLVA 153
 STIVLELSEAFILNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDD 213
 144 PISRPQVLVASTIV-LELSEAFILNCSHENGIKPSYTWLKDGKPLLNDSRMLLSPDQKVL
 DPLEGVNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKW-----QLKRDKPVTVVQSI
 269 DPVTSVPLMIEPVPRHAVEGESVLLYVH--NLPEALQTFSWYKGVYSLKEFK--IAEYSI
 Query Match
8.4%; Score 178.5; DB 2; Length 475;
Best Local Similarity 31.5%; Pred. No. 0.0011;
Matches 67; Conservative 26; Mismatches 105; Indels 15;
 3
 Length 278;
 Indels
 63;
 DB 2;
 Query Match 8.5%; Score 179.5; DB 2
Best Local Similarity 31.7%; Pred. No. 0.00046;
Matches 45; Conservative 29; Mismatches 63
 203 TITRVLMEDDDLYSCMVENPISQGRSLPVKITV 235
 440 RIHDVRREDAGQYRCEAFNPISSKTSRPVSLAV 472
 214 LYSCMVENPISQGRSLPVKITV 235
 211 EYOCEISNPVSVRRSNSIKLDI 232
 C; Keywords: glycoprotein
 A;Residues: 1-278 <MCC>
 A;Accession: A54879
 92
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 RESULT 13
S41638
T-cell surface glycoprotein CD2 precursor - horse
T-cell surface antigen CD2
T-cell surface antigen CD2
C;Species: Equus caballus (domestic horse)
C;Species: Equus caballus (domestic horse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: 341638 331578
Eur. J. Biochem. 219, 969-976, 1994
A;Title: Expression clouing of an equine T-lymphocyte glycoprotein CD2 cDNa. Structure-LA;Reference number: S41638 MUID:94155904; PMID:7906650
A;Accession: S41638
A;Accession: S41638
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A;Accession: S416
 JC1507

Joliary glycoprotein C - mouse

C;Species: Mus musculus (house mouse)

C;Species: Ausman musculus (house mouse)

C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004

C;Accession: JC1507

R;McCuaig, K.; Rosenberg, M.; Nedellec, P.; Turbide, C.; Beauchemin, N.

Gene 127, 173-183, 1993

A;Fitle: Expression of the Bgp gene and characterization of mouse colon biliary glycopro

A;Reference number: JC1505; MUID:93273228; PMID:8500759
 101 LFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLEL 160
 S1 VLKNGTLKIKHLERIHEGTYKVDAYDSDGKNVLEETFHLSLLEMVSKPNISWSCTNT--- 137
 161 SEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVE 220
 ----TLTCEVTKGTDFE---LK----LYLNGRMIQKSPRKVIVYKRASNQIAS-FKCTAN 185
 221 NPISQGRSLPVKITVYRRSSLYII--LSTGGIFLLVTLVTVCACWKPSKRKQKKLEKQNS 278
 279 LEYMDQNDDRLKPEADTLPRSGEQERKNPMALYILKDKDSPETEENPA---PEPRSATEP 335
 186 NTVSEESSSVVIRCTEKGLDIYLISGICGGGILFVFLALL--IFYISKRK-----KQNS 238
 ----RRNDEELEIRAHKV--ISEERGRKPHOI-----PGSTPLNPAASOPPPPPFPP 285
 DTF-TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNC-SHENGTKPSYTWLKDGKP 186
 33 GPPGYSVSPAVPGRSPGLP-IRSARRYPRSPARSPAT------GRTHSSPPR 380
RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITD
 LLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSSLY----
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iive 42; Mismatches 121;
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|                                                                                                                                                                                                              | AA.                             | ed)<br>sequence update)<br>annotation update)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Catarrhini; Hominidae; Homo                                                                  | A.,<br>Y.,<br>M.,<br>giyam<br>data                                                                                                                                                                                                                                  | EEICF CRC64;                                                  | DB 2; Le-114;                                                | MKRERGALSRASRALRLAPFVYLLLIOTDPLEGVNITSPVRLIHGTVGKSALLSVQXSST<br> | SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY<br> |
| 15<br>MOUSE<br>16<br>17<br>17<br>17<br>17<br>19<br>15<br>15<br>14                                                                                                                                            | MENTS<br>416                    | ed)<br>sequence update)<br>annotation updat                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | rhini;                                                                                       | K., Kumagai<br>1 M., Suzuki<br>1., Kawamura<br>1., Kawa T., Su<br>enBank/DDBJ                                                                                                                                                                                       | 47120CA9A00EE1CF                                              | 2118;<br>No. 1.1<br>matches                                  | QTDPLEG<br>       <br> QTDPLEG                                   | SVIGTLRP<br>       <br>SVIGTLRP                                  |
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| 000000000000000                                                                                                                                                                                              | •                               | 22,<br>22,<br>22,<br>26,<br>2553                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | ate                                                                                          | Mor Ke Mor Hor Hor Hor Hor Hor Hor Hor Hor Hor H                                                                                                                                                                                                                    | ii 4.<br>ΈΣ                                                   | 99.8%;<br>99.8%;<br>ive                                      | Z = Z                                                            | ¥=¥                                                              |
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|                                                                                                                                                                                                              | RELI                            | Tremblr<br>Tremblr<br>Tremblr<br>Protein<br>(Human)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | neric<br>06;<br>N.A                                                                          | Y., Yamazaki<br>X., Fujimori<br>K., Mizuno S<br>Octsuki T.,<br>Isogai T.,<br>IUL-2002)<br>98396; BAC05<br>IPR007110,                                                                                                                                                | 835;<br>835;                                                  | arity<br>onse                                                | SGALS<br>                                                        | PWK9                                                             |
|                                                                                                                                                                                                              |                                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Eut)<br>=96(<br>ROM                                                                          | 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                                                                                                                                                                                                                               | \$508<br>\$508<br>416                                         | m113                                                         | KREI<br>KREI                                                     | SDR1                                                             |
| 189<br>188.5<br>187.5<br>187.5<br>187.5<br>187.5<br>187.5<br>186.5<br>186.1<br>186<br>186<br>186                                                                                                             | JT 1<br>13<br>Q8N713<br>Q8N713; | 01-OCT_2002 (TrEMBL:<br>01-OCT-2002 (TrEMBL:<br>01-MRR-2004 (TrEMBL:<br>Hypothetical protein<br>Homo agapiens (Human)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | bukalyota, merazoa,<br>Mammalia, Eutheria,<br>NCBI TaxID=9606;<br>[1]<br>SEQUENCE, FROM N.A. | Tabhiro H., Yamazaki M., Wata<br>Fukuzumi. Y., Fujimori Y., Kom<br>Nakagawa Ki., Mizuno S., Morin<br>Irie R., Otsuki T., Suco H.,<br>Nagai K., Isogai T., Sugano S<br>Submitted (JUL-2002) to the E<br>EMBL; AKO98396; BACO5297.1;<br>InnerPro; IPR00;110; Ig-11ke. | FIGURAL SECURATION OF THE STREET SECURATE SECURACE 416 AA; 45 | Query Match<br>Best Local Similarity<br>Matches 415; Conserv | η η<br>Σ—Σ                                                       | 61 S<br>61 S                                                     |
| ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~                                                                                                                                                                       | 7LT 1<br>713<br>Q8N<br>Q8N      | 001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1-001-1- | Mamma<br>NCBI<br>[1]<br>SEQUI                                                                | Nak<br>Nak<br>Nag<br>Subb                                                                                                                                                                                                                                           | SWA<br>PRO<br>SEO                                             | ery<br>set L                                                 |                                                                  |                                                                  |
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241 LYIILSTGGIFLLVTLVTVCACWKPSKRKQKKLBKQNSLEYMDQNDDRLKPEADTLPRSG 300 EQERKNPMALYILKDKDSPETEENPAPEPRSATEPGPPGYSVSPAVPGRSPGLPIRSARR 360

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181 LKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCVVENPISQGRSLPVKITVYRRSS

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InterPro; IPR003299; Ig.
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Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

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Rohack S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Anithing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Raywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

Jones S.J., Marra M.A.,

Tand mouse CDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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 RKNPMALYILKDKDSPETEENPAPEPRSATEPGPPGYSVSPAVPGRSPGLPIRSARRYPR 363
 9
 126 ITDDTFTGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGK
 STGGI FLLVTLVTVCACWKPSK - - RKQKKLEKQNSLEYMDQNDDRLKPEADTLPRSGEQE
 241 STGGIPLLVTLVTVTVCACWKPSKKSRKKRKLEKQNSLEYMDQNDDRLKSEADTLPRSGEQE
 66 VVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTYEVEIS
 PLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSSLYIIL
 GALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSSTSSDRP
 SPARSPATGRTHSSPPRAPSSPGRSRSASRTLRTAGVHIIREQDEAGPVEISA 416
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 5;
 Length 413;
 SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
Director MGC Project;
Submitted (EEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC082537; AAH82537.1; -.
 413 AA; 45665 MW; B6EFCA2D6D2CA3C1 CRC64;
Q640R3;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
2900042E01Rik protein (Fragment).
 92.7%; Score 1967; DB 2; 94.2%; Pred. No. 6.1e-106; iive 10; Mismatches 12;
 Best Local Similarity 94.2%
Matches 389; Conservative
 Mus musculus (Mouse)
 NCBI_TaxID=10090;
 364
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165 AA

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PRELIMINARY;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 TISSUE=Brain;
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 Suzuki O., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Shiohata N.,
A Buzuki O., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Shiohata N.,
A Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,
A Matsumuta S., Satoh N., Matsumawa H., Takahashi E., Kataoka R.,
A Kaeriyama S., Satoh I., Kamata K., Takami S., Terashima Y.,
A Karanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T.,
A Makamatsu A., Ishii S., Yamanoto J., Isono Y., Kawai-Hio Y., Saito K.,
A Nishikawa T., Ximura K., Yamashita H., Matsuo K., Nakamura Y.,
A Sakine M., Kikuchi H., Kanda K., Waqatsuma M., Murakawa K.,
Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AK122595, BAC85486.1; --
COCO004872; Freceptor activity; IEA.
 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDSRDRIRLFENGSLLLSDLQLADEGTY 120
 LKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCVVENPISQGRSLPVKITVYRRSS 240
 SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY 120
 EVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTW 180
 181 LKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSS 240
 241 LYIILSTGGIFLLVTLVTVCACWKPSKRKQKKLEKQNSLEYMDQNDDRLKPEADTLPRSG 300
 241 LYIILSTGGIFLLVTLVTVCACWKPSKRKQKKLEKQNSLEYMDQNDDRLKPEGE-LPAT- 298
 EQERKNPMALYI-----LKDKDSPETEENPAPEPRS-ATEPGPPGYSVSPAVPGR 349
 1 MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNIT3BPVRLIHGTVGKSALLSVQYSST 60
 1 MKRERGALSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST
 / Match 69.7%; Score 1478.5; DB 2; Length 367; Local Similarity 84.7%; Pred. No. 9.5e-78; nes 305; Conservative 12; Mismatches 26; Indels 17; Gaps
361 SPARSPATGRTHTSPPRAPSSPGRSRSSRSLRTAGVQRIREQDESGQVEISA 413
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 367 AA; 40456 MW; 35956FA245A408F0 CRC64;
 05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ16002.
Homo sapiens (Human).
 InterPro; IPR003599; IG.
InterPro; IPR007110; IG-like.
InterPro; IPR003598; IG_C2.
Ffam; PF00047; Ig; 1.
SMART; SM00409; IG; 2.
SMART; SM00409; IG. 2.
 PROSITE; PS50835; IG_LIKE; 1.
 PRELIMINARY;
 SEQUENCE FROM N.A.
 SEQUENCE
 121
 19
 181
 301
 Query Match
 Q6ZWL4
 Matches
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RESULT Q8ND35

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60 YILKDKDSPETEENPAPEPRSATEPGPPGYSVSPAVPGRSPGLPIRSARRYPRSPARSPA 119
 311 YILKDKDSPETEENPAPEPRSATEPGPPGYSVSPAVPGRSPGLPIRSARRYPRSPARSPA
 1 FLLVTLVTVCACWKPSKRKQKKLEKQNSLEYMDQNDDRLKPE-DTLPRSGEGERKNPMAL
 251 FLLVTLVTVCACWKPSKRKQKKLEKQNSLEYMDQNDDRLKPEADTLPRSGEQERKNPMAL
 MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Clen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Baton D., Poster J., Grimaldi C., Gu Q., Hase P.E., Heldens S., Huang A., Kilm, H.S., Kilmowski L., Jin Y., Johnson S., Lee J., Seshagiri S., Simmons L., Singh J., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P.;
 Gaps
 "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: bioinformatics assessment."; Genome Res. 13:226-2270(2003).
EMBL, AX36345; AAG88711.1; -.
InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003599; Ig.
SMART; SM00409; IG; 1.
 ORFNames=UNQ305;

Momo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Euteleostomi;
 Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Wiemann Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, ALB34419; CAD39081.1; -.
 ۲,
 Query Match
40.3%; Score 854.5; DB 2; Length 165;
Best Local Similarity 99.4%; Pred. No. 4.3e-42;
Matches 165; Conservative 0; Mismatches 0; Indels 1;
 371 TGRTHSSPPRAPSSPGRSRSASRTLRTAGVHIIREQDEAGPVEISA 416
 TGRTHSSPPRAPSSPGRSRSASRTLRTAGVHIIREQDEAGPVEISA 165
 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Hypothetical protein.
NON TER 1 1 SEQUENCE 165 AA; 18161 MW; 5052FA978C437486 CRC64;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
Hypothetical protein DKFZp5470159 (Fragment).
 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 PRELIMINARY;
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242 -----RRNDEELEIRAH---RAATEERGKKPHQIPASTPQNPAASQHPPPPPGHRSQAP 292
218 MVENPISQGRSLPVKITVYRRSSLYIILS-TGGIFLLVTLVTVCACWKPSKRKQKKLEKQ 276
 186 TAGNKVSKESRVETVSCTEKGLDIYLIIGICGGGSLLMVFVTLLVFYITKRKKQRS---- 241
 277 NSLEYMDQNDDRLKPEADTLPRSGEQERKNPMALYILKDKDSPETEENPAPEPRSATE-- 334
 293 SHRPLPPGHRVQHQPQKRPPAPSGTQVHQQKGPPLPRPRVQPKPPQGAAENSLSPSS 349
 335 ---PGPPGYSVS-----PAVPG----RSPGLPIRSARRYPRSPARSPATGRTHSS 377
 MEDLINE=87204243; PubMed=2883656;
Sayre P.H., Chang H.-C., Hussey R.E., Brown N.R., Richardson N.E.,
Spagnoli G., Clayron L.K., Reinherz E.L.;
"Molecular cloning and expression of Til cDNAs reveal a receptor-like
structure on human T lymphocytes.";
Proc. Natl. Acad. Sci. U.S.A. 84:2941-2945(1987).
 The structure of the human CD2 gene and its expression in transgenic
 human and murine
 T-call surface antigen CD2 precursor (T-cell surface antigen T11/Leu-5) (LFA-2) (LFA-3 receptor) (Erythrocyte receptor) (Rosette receptor)
 MEDLINE-89005055; PubMed-2901953;
Lang G., Wotton D., Owen M.J., Sewell W.A., Brown M.H., Mason D.Y.,
Crumpton M.J., Kioussis D.;
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 erythrocyte
 Sewell W.A., Brown M.H., Dunne J., Owen M.J., Crumpton M.J., Proc. Natl. Acad. Sci. U.S.A. 84:7256-7256(1987).
 SEQUENCE FROM N.A., AND VARIANT HIS-266.
Hall R.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
[8]
 Sewell W.A., Brown M.H., Dunne J., Owen M.J., Crumpton "Molecular cloning of the human T-lymphocyte surface CI
 Diamond D.J., Clayton L.K., Sayre P.H., Reinherz B.L., "Exon-intron organization and sequence comparison of h
 Seed B., Aruffo A.;
"Molecular cloning of the CD2 antigen, the T-cell recepture, by a rapid immunoselection procedure.", proc. Natl. Acad. Sci. U.S.A. 84:3365-3369(1987).
 T11 (CD2) genes.";
Proc. Natl. Acad. Sci. U.S.A. 85:1615-1619(1988).
 Proc. Natl. Acad. Sci. U.S.A. 83:8718-8722(1986)
 P06729, Q96TE5;
01-JNN-1988 (Rel. 06, Created)
01-NOV-1988 (Rel. 06, Last sequence update)
T-cell surface antigen CD2 precursor (T-cell s
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 351
 SEQUENCE FROM N.A., AND VARIANT HIS-266.
 SEQUENCE FROM N.A., AND VARIANT HIS-266.
MEDLINE=88144486; Pubmed=2894031;
 SEQUENCE FROM N.A., AND VARIANT HIS-266.
MEDLINE-87041523; Pubmed=3490670;
 PRT;
 SEQUENCE FROM N.A.
MEDLINE=87204137; PubMed=2437578;
 STANDARD;
 Homo sapiens (Human)
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 HUMAN
 REVISIONS
 (CD2)
 Name=CD2
 antigen.
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 CD2_HUMAN
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 13;
 62 HTMPKYLLGSVNKSVVDDL--EYQHKFTMMPDNASLLINPLQFPDEGNYIVKVNIQGNGT 119
 45 GTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP----DYRDRIR 100
 101 LFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLEL 160
 161 SEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLT---ITRVLMEDDDLYSC 217
 74 -DKPVTVVQSIGTEVIGTLRPDYRDRIRLF-ENGSLLLSDLQLADEGTYEVEISIT-DDT 130
 131 FTGEKTINLTVDVPISRPQVLV-ASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLN 189
 61
 3 LKVFTTFLSFATGACSGLKVTVPSHTVHGVRGQALYLPVHYGFHTPASDIQII-WLFERP
 17 LAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYS--STSSDRPVVKWQLKR-
 Damschroder M.M., Kozhich A.A., Woods R.M., Cheng L., Mullikin B.A., Wilson S.D., Ulbrandt N.D., Bachy C.M., Wu H., Suzich J.A., Kiener P.A., Dall'Acqua W.F., White W.I.;

"Analysis of human and primate CD2 molecules by protein sequence and epitope mapping with anti-human CD2 antibodies.";

Mol. Immunol. 41:985-1000(2004).

EMBL, AV45038; AAR15885.1; -.

HSSP, P08921; 1A64.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:00155; P:cell adhesion; IEA.

InterPro; IPR008424; CD2.

InterPro; IPR001110; Ig-like.

Pfam; PP05790; C2-set; 1.
 Gaps
 Gaps
 Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).

Bukaryota, Metazoa; Chordata; Craniata, Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Cercocebus.
 :99
 10;
 190 DSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVY 236
 SSTYSFSPQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIY 226
 Length 450;
 Length 350;
 10.6%; Score 224; DB 2; Length 35
23.5%; Pred. No. 3.2e-05;
.ive 61; Mismatches 146; Indels
 ; Score 282; DB 2; Length 45; Pred. No. 2e-08; 43; Mismatches 102; Indels
 SMART; SM00408; IGC2; 1.
PROSITE; PS50835; IG LIKE; 2.
SEQUENCE 450 AA; 50114 MW; A22FF822CC3CB226 CRC64;
 350 AA; 39493 MW; 621C74BC81D8C95D CRC64;
 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 350
 PRT;
 Cluster of differentiation 2.
 13.3%;
 Duery Match
Best Local Similarity 23.54
Matches 84; Conservative
 Conservative
 PRELIMINARY;
 Query Match
Best Local Similarity
72; Conserve
 SEQUENCE FROM N.A.
 PubMed=15302161;
 85
 142
 SEQUENCE
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Pfam; PF05790; CD2; 1.
 PIR; A28967; RWHUC2
PDB; 1CDB; NMR; @=2
 ransmembrane.
 CARBOHYD
 'RANSMEM
 DISULPID
 DISULFID
 CARBOHYD
 MUTAGEN
MUTAGEN
MUTAGEN
 SIGNAL
CHAIN
DOMAIN
 DOMAIN
DOMAIN
DOMAIN
 VARIANT
 MUTAGEN
 DOMAIN
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 DOMAIN
 EMBL;
 MEDINE-2018625, PubMed=11477912; DOI=10.1073/pnas.242601899; MEDINE-2018825; PubMed=11477912; DOI=10.1073/pnas.242601899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heng J., Heibe F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brapleton M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Hilton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Hilton M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C., Schmutz J., Myers R.M., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones C., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones C., Shereztion and initial analysis of more than 15,000 full-length human
 MEDLINE=92311658; PubMed=1377404;
Hahn W.C., Menu E., Bothwell A.L.M., Sims P.J., Bierer B.E.;
Woverlapping but nonidentical binding sites on CD2 for CD58 and a second ligand CD59.";
Science 256:1805-1807(1992).
-!- FUNCTION: CD2 interacts with lymphocyte function-associated antigen (LFA-3) and CD48/BCM1 to mediate adhesion between T cells and other cell types. CD2 is implicated in the triggerring of T-cells, the cytoplasmic domain is implicated in the signaling
 STRUCTURE BY NMR OF 25-129.
MEDLINE=94348865; PubMed=7915183; DOI=10.1016/0969-2126(93)90009-6;
Withka J.M., Wyss D.F., Wagner G., Arulanandam A.R.N., Reinherz E.L.,
 Recny M.A.; \pi "Structure of the glycosylated adhesion domain of human T lymphocyte
 MEDLINE=95381065; PubMed=7544493; Wyss D.F., Choi J.S., Li J., Knoppers M.H., Willis K.J., Arulanandam A.R., Smolyar A., Reinherz E.L., Wagner G.; "Conformation and function of the N-linked glycan in the adhesion domain of human CD2."; Science 269:1273-1278 (1995).
 MEDLINE-95086863; PubMed-7994575;
Bodian D.L., Jones B.Y., Harlos K., Stuart D.I., Davis S.J.;
"Crygtal structure of the extracellular region of the human cell
adhesion molecule CD2 at 2.5-A resolution.";
Structure 2:755-766(1994).
 SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
DATABASE: NAME-EROW; NOTE=CD guide CD2 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd2.htm".
 MEDLINE-88039075; PubMed=2444890; DOI=10.1038/329842a0; Peterson A., Seed B.; "Monoclonal antibody and ligand binding sites of the T cell erythrocyte receptor (CD2).";
 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 SUBUNIT: Interacts with CD2AP (By similarity).
 K-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 25-206.
 STRUCTURE BY NMR OF 25-129
 Nature 329:842-846(1987).
 Structure 1:69-81(1993).
 CD59-BINDING DATA.
SEQUENCE FROM N.A.
 glycoprotein CD2
 function.
 MUTAGENESIS.
 100
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
 12;
 .; NAS.
 Gaps
 N-linked (GlcNAc.) (Potential).

Q -> H (in dbSNP:699738).

Y-TIG=VAR. 07104.

K-XR: Loss of LPA-3 binding.

Q -> K: Loss of LPA-3 binding.

Y-D: Loss of LPA-3 and CD59 binding.

D->H: Loss of LPA-3 and CD59 binding.
 CO; GC:0005515; F:proced binding; IPI.

CO; GC:0004872; F:receptor activity, NAS.

CO; GC:0001665; P:cell surface receptor linked signal transdu...

CO; GC:0001637; P:cell adhesion; NAS.

CO; GC:0001766; P:lipid raft polarization; TAS.

CO; GC:0001766; P:lipid raft polarization; TAS.

CO; GC:0001766; P:lipid raft polarization; TAS.

CO; GC:0001767; P:lipid regulation of dendritic cell activ...

CO; GC:0001017; P:regulation of T-cell differentiation; NAS.

CO; GC:00042110; P:T-cell activation; TAS.

InterPro; IPR008424; CD2.
 62;
 By similarity.
By similarity.
N-linked (GlcNAc. .). (Potential)
N-linked (GlcNAc. .) (Potential)
N-linked (GlcNAc. .) (Potential)
 T-cell surface antigen CD2.
Extracellular (Potential).
Potential.
Cytoplasmic (Potential).
Ig-like V-type.
Ig-like C2-type.
IRA-3 (CD58) binding region 1.
IRA-3 (CD58) binding region 2.
 PROSÍTE; PS50815; IG LIKE; FALSE NEG.
3D-structure; Antigen; Cell adhesion; Glycoprotein;
Immunoglobulin domain; Polymorphism; Repeat; Signal; T-cell;
 Score 221; DB 1; Length 351; Pred. No. 4.8e-05;
 60; Mismatches 164; Indels
 GO; GO:0005887; C:integral to plasma membrane; NAS.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0004872; F:receptor activity; NAS.
 Pro-rich.
 EMBL; M14362; AAA35571.1; EMBL; M16336; AAA51946.1; EMBL; M19806; AAA53095.1; JUNED. EMBL; M19800; AAA53095.1; JOINED. EMBL; M19800; AAA53095.1; JOINED. EMBL; M19804; AAA53095.1; JOINED. EMBL; X07871; CAA30721.1; JOINED. EMBL; X07872; CAA30721.1; JOINED. EMBL; X07873; CAA30721.1; JOINED. EMBL; X07873; CAA30721.1; JOINED. EMBL; X07873; CAA30721.1; JOINED.
 10.4%;
22.9%;
 AL135798; CAC14840.1;
BC033583; AAH33583.1;
 1HNF; X-ray; @=25-206.
1L2Z; NMR; B=294-304.
 Conservative
 1CDB; NMR; @=25-129.
1GYA; NMR; @=25-129.
 GlycosuiteDB; P06729; -
Genew; HGNC:1639; CD2.
H-InvDB; HIXO000931; -.
MIM; 186990; -.
 Best Local Similarity
Matches 85; Conserv
 Query Match
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last seq
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 PRELIMINARY;
 Cercopithecinae, Papio.
 (TrEMBLrel
 Local Similarity
wes 80; Conserv
 SEQUENCE FROM N.A.
 NCBI TaxID=9555,
 05-JUL-2004
 Name=CD2;
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 Gaps 11;
 192 RMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSSLYIILS-TGGI 250
 251 FLLVTLVTVCACWKPSKRKQKKLEKQNSLEYMDQNDDRLKPEADTLPRSGEQERKNPMAL 310
 77 VTVVQSIGTEVIGTLRPD----YRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTF 131
 -----KKIAQFRKEKETFKEKDTYKLFKNGTLKIKHLKTDDQDIYKVSIYDTKGKN 116
 132 TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDS 191
 SLIMVFVALLVFYITKRKKÖRS-----RRNDEELETRAH---RVATEERGRKPQQ 267
 311 YILKOKDSPETEENPAPEPRSATE----PGPPGYSVS-----PAVPG----RSPGLP 354
 65
 GALGODIDLDIPSFOMSDDIDDIKWEKTSDK------KKIAQFRKEKETFEEKDAY 84
 GTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP----DYRDRI
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 PubMed=15302161;
Damschroder M.M., Kozhich A.A., Woods R.M., Cheng L., Mullikin B.A., Wilson S.D., Ulbrandt N.D., Bachy C.M., Wu H., Suzich J.A., Wilson S.D., Ulbrandt N.D., Bachy C.M., Wu H., Suzich J.A., "Analysis of human and primate CD2 molecules by protein sequence and epitope mapping with anti-human CD2 antibodies.";
Mol. Immunol. 41:985-1000(2004).
HSSP: P08921: 1A64
 Macaca assamensis (Assam's macaque) (Assam's monkey).
Walkaryota; Metacoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
 61;
 DB 2; Length 345;
 Indels
 063DF110344542A7 CRC64;
 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Cluster of differentiation 2 (Fragment).
 / Match 10.2%; Score 217.5; DB 2; Local Similarity 23.3%; Pred. No. 7.6e-05; nes 80; Conservative 54; Mismatches 148;
 GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR008424; CD².
InterPro; IPR007110; IG-like.
 345 AA
 PRT;
 345 AA; 38952 MW;
 : | |: |
328 LPRPRVQPKPP 338
 355 IRSARRYPRSP 365
 PRELIMINARY;
 Pfam; PF05790; C2-set;
 SEQUENCE FROM N.A.
 NCBI_TaxID=9551;
 345
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SEQUENCE
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 Query Match
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85 KLFKNGTLKIKHLKIHDQDSYKVSIYDTKGKNVLEKTFDLKIQERVSEPKI---SWTCIN 141
 160 LSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMV 219
 220 ENPISOGRSLPVKITVYRRSSLYIILS-TGGIFLLVTLVTVCACWKPSKRKOKKLEKONS 278
 279 LEYMDQNDDRLKPEADTLPRSGEQERKNPMALYILKDKDSPETEENPAPEPRSATE---- 334
 220 ENPISQGRSLPVKITVYRRSSLYIILS-TGGIFLLVTLVTVCACWKPSKRKQKKLEKQNS 278
 160 LSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRMLLSPDQKVLTITRVLMEDDDLYSCMV 219
 142 T----TLTCEVANGTDPELNLYQDGKHLKLSQRVITHKWTTSLSAK------FKCTA 188
KLFKNGTLKIKHLKIHDQDSYKVSIYDTKGKNVLEKTFDLKIQERVSEPKI---SWTCIN 141
 99
 84
 35 GALGODIDLDIPSFOMSDDIDDIKWEKTSDK-----KKIAOFRKEKETFEEKDAY
 100 RLFENGSILLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLE
 142 T----TLTCEVMNGTDPELNLYQDGKHLKLSQRVITHKWTTSLSAK------FKCTA
 GTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP----DYRDRI
 279 LEYMDQNDDRLKPEADTLPRSGEQERKNPMALYILKDKDSPETEENPAPEPRSATE----
 189 GNKVSKESRMETVSCPEKGLDIYLIIGICGGGSLLMVFVALLVFYITKRKKÖRS-----
 Pumicharian, Kozhich A.A., Woods R.M., Cheng L., Mullikin B.A., Wilson S.D., Ulbrandt N.D., Bachy C.M., Wu H., Suzich J.A., Kaner B.A., Dall'Acqua W.F., Milte W.I.;

Analysis of human and primate DDE W.I.;

"Analysis of human and primate CD2 molecules by protein sequence and epitope mapping with anti-human CD2 antibodies.";

MOI. Immunol. 41:985-1000(2004).

EMBL; AV45035; AAR15882.1; -.

HSSP; P08921; LA64.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:00155; P:cell adhesion; IEA.

InterPro; IPR009424; CD2.

InterPro; IPR004424; CD2.

Pfam; PF05790; C2-set; 1.
 Gaps
 Papio anubis (Olive baboon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae;
 61;
 Length
 Indels
 -PGPPGYSVS-----PAVPG----RSPGLPIRSARRYPRSP 365
 296 келерсикуонороккерарызстоинооксертекторите
 344 AA; 38916 MW; 063CF2A3869E5BA6 CRC64;
 Last sequence update)
Last annotation update)
 10.2%; Score 215.5; DB 2; 23.3%; Pred. No. 9.8e-05; tive 54; Mismatches 148;
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 Cluster of differentiation 2 (Fragment)
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251 FLLVTLVTVCACWKPSKRKQKKLEKQNSLEYMDQNDDRLKPEADTLPRSGEQERKNPMAL 310
 131
 RMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSSLYIILS-TGGI 250
 RVITHKWITSLSAK------FKCTAGNKVSKESSVEPVSCPEKGLDIYLIIGICGGG 220
 221 SLLMVFVALLVFYITKRKKQRS------RRNDEELETRAH---RVATEERGRKPHQ 267
 311 YILKDKDSPETEENPAPEPRSATE-----PGPPGYSVS-----PAVPG----RSPGLP 354
 268 IPASTPQNPAASQHPPPPPPGHRSQAPSHRPPPPGHRVQHQPQKRPPAPSGTQVHQQKGPP 327
 92
 65
 77 VTVVQSIGTEVIGTLRPD-----YRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTF
 17 LAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKP
 8 VASFLLIFNVSSKGAVSEEITNALE-TWGALGQDINLDIPSFQMSDDIDDIKWEKTSDK-
 132 TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDS
 Damschroder M.M., Kozhich A.A., Woods R.M., Cheng L., Mullikin B.A., Wilson S.D., Ulbrandt N.D., Bachy C.M., Wu H., Suzich J.A., Kiener P.A., Dall'Acqua W.F., White W.I.; "Analysis of human and primate CD2 molecules by protein sequence and epitope mapping with anti-human CD2 antibodies."; Mol. Immunol. 41:985-1000(2004).

EMBL, AY445034; AAR15881.1; -.
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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 62;
 Length 345;
 Query Match
10.1%; Score 215; DB 2; Length 34:
Best Local Similarity 22.6%; Pred. No. 0.00011;
Matches 84; Conservative 60; Mismatches 165; Indels
 296 RPLPPGHRVOHOPOKRPPAPSGTQVHQOKGPPLPRPRVQPKPP 338
 CRC64;
 335 -PGPPGYSVS-----PAVPG----RSPGLPIRSARRYPRSP
 Last sequence update)
Last annotation update)
 6B23B5AC3A57C3C7
 Z
 GO, GO:0016021, C:integral to membrane; IEA.
GO; GO:0007155, P:cell adhesion; IEA.
InterPro; IPR008424; CD2.
InterPro; IPR0007110; IG-like.
 5-JUL-2004 (TrEMBLrel. 27, Last annotat. luster of differentiation 2 (Fragment).
 Created)
 PRT;
 345 345
345 AA; 38833 MW;
 Pan troglodytes (Chimpanzee)
 (TrEMBLrel. 27, (TrEMBLrel. 27,
 PRELIMINARY;
 355 IRSARRYPRSP 365
 : | |: |
328 LPRPRVQPKPP 338
 Pfam; PF05790; C2-set;
 P08921; 1A64.
 SEQUENCE FROM N.A. PubMed=15302161;
 345
 05-JUL-2004
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 243
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14;
 132 T----TLTCEVMNGTDPELNLYQDGK-----HVKLS--QRVITHKWTTSLSAK----FK 175
 217 CMVENPISQGRSLPVKITVYRRSSLYIILS-TGGIFLLVTLVTVCACWKPSKRKQKKLEK 275
 276 ONSLEYMDONDDRLKPEADTLPRSGEQERKNPMALYILKDKDSPETEENPAPEPRSATE- 334
 74
 25 GALGODIDLDIPSFOMSDDIDDIKWEKTSDK------KKİAQFRKEKETFEEKDAY
 100 RLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEXTINLTVDVPISRPQVLVASTTVLE
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 67; Gaps
 and
 B.A.,
 Euteleostomi;
 PubMed=15302161;
Damschroder M.M., Kozhich A.A., Woods R.M., Cheng L., Mullikin B..
Wilson S.D., Ulbrandt N.D., Bachy C.M., Wu H., Suzich J.A.,
Kiener P.A., Dall'Acqua W.F., White W.I.;
"Analysis of human and primate CD2 molecules by protein sequence epicope mapping with anti-human CD2 antibodies.";
EMBL; AY445041; AAR1S888.1; --.
HSSP; P08921; 1A64.
 10.0%; Score 212.5; DB 2; Length 334; 24.0%; Pred. No. 0.00014; rive 56; Mismatches 140; Indels 67;
 335 ----PGPPGYSVS-----PAVPG----RSPGLPIRSARRYPRSP 365
 рѕнкріреснкуднорожкераростоуноджоргереру
 Macaca nemestrina (Pig-tailed macaque).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
 334 AA; 37781 MW; EBSF8378B099D80F CRC64;
 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Cluster of differentiation 2 (Fragment).
 Last sequence update)
Last annotation update)
334 AA
 GO, GO:0016021, C:integral to membrane, IEA. GO; GO:0007155; P:cell adhesion; IEA.
 341
 05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequen
05-UUL-2004 (TrEMBLrel. 27, Last annota
05-UUL-2004 (TrEMBLrel. 27, Last annota
Cluster of differentiation 2 (Fragment)
 Macaca arctoides (Stump-tailed macague)
PRT;
 PRT;
 InterPro; IPR008424; CD2.
InterPro; IPR007110; Ig-like.
 Query Match
Best Local Similarity 24.v.,
Best Local 83; Conservative
PRELIMINARY;
 PRELIMINARY;
 Pfam; PF05790; C2-set;
 334
 SEQUENCE FROM N.A.
 NCBI TaxID=9545;
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 186 CTAGNKVSKESRMETVSCPEKGLDIYLIIGICGGGSLLMVFVALLVFYITKRKKQRS--- 242
 100 RLFENGSLLLSDLQLADEGTYEVEISITDDTFTGEKTINLTVDVPISRPQVLVASTTVLE 159
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 217 CMVENPISQGRSLPVKITVYRRSSLYIILS-TGGIFLLVTLVTVCACWKPSKRKQKKLEK 275
 276 QNSLEYMDQNDDRLKPEADTLPRSGEQERKNPMALYILKDKDSPETEENPAPEPRSATE- 334
 243 -----RRNDEELEIRÄH---RVATEERGRKPHQIPASTPQNPAASQHPPPPPFGHRSQA 292
 Damschroder M.M., Kozhich A.A., Woods R.M., Cheng L., Mullikin B.A., A Wilson S.D., Ulbrandt N.D., Bachy C.M., Wu H., Suzich J.A., Kiener P.A., Dall'Acqua W.F., White W.I., analysis of human and primate CD2 molecules by protein sequence and T. "Analysis of human and primate CD2 molecules by protein sequence and prince mapping with anti-human CD2 antibodies."; photope mapping with anti-human CD2 antibodies."; Photope mapping with anti-human CD2 antibodies."; REMBL, AY445040; AAR15887.1; -...
REMBL, AY445040; AAR15887.1; -...
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ROG GO:000155; P:cell adhesion; IEA.
ROG GO:0007155; P:cell adhesion; IEA.
RICEPRO; IPR00110; Ig-like.
R Pfeam; PF05790; CZ-set; 1.
 45 GTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRP----DYRDRI 99
 | : | : | : | : | 35 GALGQDIDLDIPSFQMSDDIDDIKWEKTSDK------KKIAQFRKEKETFEEKDAY 84
 Gaps
 STRAIN=CD1; TISSUE=Colon; MEDLINE=93273228; PubMed=8500759; DOI=10.1016/0378-1119(93)90716-G; MEDLINE=93273228; PubMed=8500759; DOI=10.1016/0378-1119(93)90716-G; MCCuaig K., Rosenberg M., Turbide C., Beauchemin N., Nedellec P.; McCuaig K., Rosenberg M., Turbide C., Beauchemin N., Nedellec P.; Expression of the Bgp gene and characterization of mouse colon billary glycoprotein isoforms."; Gene 127:173-183(1993).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
 67;
 10.0%; Score 212.5; DB 2; Length 341; 24.0%; Pred. No. 0.00014; ive 56; Mismatches 140; Indels 67
 335 ----PGPPGYSVS-----PAVPG----RSPGLPIRSARRYPRSP 365
 293 РЅНКРІРРСНКУОНОРОККРРАРЅСТОVНООКСРРІРКРКУОРКРР 338
 341 AA; 38565 MW; DFAC90E8247194A6 CRC64;
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Biliary glycoprotein precursor.
Name=Ceacani; Synonyms=Bgph;
Mus musculus (Mouse)
 341 AA
 PRT;
 24.0%;
 83; Conservative
 PRELIMINARY;
 Best Local Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=9540;
 PubMed=15302161;
 SEQUENCE
 Query Match
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73 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITD 128
 69 KGNPVSTNABİVHFVTGİNKTTTGPAHSGRETVYSNGSLLIQRVTVKDTGVYTIE--MTD 126
 DIF-TGEKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPL 187
 245 ---LSTG-----GIFLLVTLVTVCACWKPSKRKOKKLEKONSLEYMDONDDRLKPEAD 294
 188 INDSRMLLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSSLYII---
 34; Gaps
 "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: bioinformatics assessment.";

Bioinformatics assessment.";

EMBL, AX358084; AAQ88451.1; -.

InterPro; IPR003599; IG.

InterPro; IPR003599; IG.

InterPro; IPR003598; Ig.

InterPro; IPR003598; Ig.-2.
 Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P. Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Ssembagiri S., Simonns L., Singy J., Smith V., Stinson J., Vagts A., Vandlen R., Wateanabe C., Wheand D., Woods K., Xie M.H., Yansura D., Xi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Length 341;
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MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
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9.9%; Score 211; DB 2; Length 34
Best Local Similarity 26.1%; Pred. No. 0.00018;
Matches 73; Conservative 47; Mismatches 126; Indels
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SEQUENCE 341 AA, 36901 MW, B5278D6606996341 CRC64;
 295 TLPRSGEQERKNPMALYILKDKDSPETEENPAPEPRSATE 334
 Last sequence update)
Last annotation update)
 Created)
 PRT;
 PIR, JG1512, JG1512.
HSSP, O61353, 1162.
MGD, MG1.1347245, Ceacaml.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
Fram, Pro0047, ig; 1.
SMART; SMO408; IG2; 1.
PROSITE; PS50835, IG_LIKE; 1.
 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
EMBL; X67283; CAA47700.1;
 PRELIMINARY;
 Pfam; PF00047; ig; 1.
SMART; SM00409; IG; 2.
 Homo sapiens (Human)
 ORFNames=UNQ3098;
 NCBI_TaxID=9606;
 Yi S., Yu G.,
Godowski P.;
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9;
 78 TVVQSIGTEVIGT-LR---PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITDDTFTG 133
 74 EPNOLIAAYVIDTHVRTPGPAYSGRETISPSGDLHFONVTLEDTGYYNLQVTYRNSQIE- 132
 134 EKTINLTVDVPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTWLKDGKPLLNDSRM 193
 194 LLSPDQKVLTITRVLMEDDDLYSCMVENPISQGRSLPVKITVYRRSSLYIILSTGGIFLL 253
 18 APFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSSTSSDRPVVKWQLKRDKPV 77
 Gaps
 248 SLLVAALVCF-----LLLRKTGRASDQSDFREQQPPASTPGHGPSD 288
 Query Match
9.9%; Score 210.5; DB 2; Length 292;
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Matches 79; Conservative 47; Mismatches 129; Indels 35;
 254 VTLVTVCACWKPSKRKQKKLEKQNSLEYMDQNDDRLKPEADTLPRSGEQE 303
SMART; SM00408; IGc2; 1.
PROSITE; PS50835; IG LIKE; 1.
SEQUENCE 292 AA; 32315 MW; 2D4DE7851E301C57 CRC64;
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